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## (FILE 'HOME' ENTERED AT 09:40:57 ON 15 JUN 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT

09:41:28 ON 15 JUN 2004

- L1 1631 S HUMAN PROTEIN C
- L2 11812 S PROTEIN C (P) HUMAN
- L3 11815 S L1 OR L2
- L4 9890993 S VARIANT OR MUTANT OR FRAGMENT OR MUTAT? OR SUBSTITUT? OR DELE
- L5 3991 S L3 (P) L4
- L6 293 S K251 OR LYS 251 OR (RESIDUE 251) OR (POSITION 251)
- L7 0 S L5 (P) L6
- L8 100458 S PROTEIN C
- L9 18051 S L8 (P) L4
- L10 1 S L9 (P) L6
- L11 10786 S ANTICOAGULANT ACTIVITY
- L12 3796 S AMIDOLYTIC ACTIVITY
- L13 6976 S ALPH-1-ANTITRYPSIN OR (ALPHA-1 PI) OR (ALPHA-1

## PROTEINASE INH

- L14 2688 S (HUMAN PLASMA) (P) INACTIVAT?
- L15 4254894 S (IN VITRO) OR (IN VIVO)
- L16 34385 S L15 (P) (HALF-LIFE)
- L17 288 S L5 (P) (L11 OR L12)
- L18 80 S L5 (P) (L13 OR L14)
- L19 30 S L5 (P) L16
- L20 339 S L17 OR L18 OR L19
- L21 0 S L20 AND L6
- L22 0 S K251G OR K251S OR K251T OR K251C OR K251Y OR K251N OR

## K251Q

- L23 14938 S ANDERSON K?/AU
- L24 2638 S PEDERSEN A?/AU
- L25 17 S FRESKGAARD P?/AU
- L26 17590 S L23 OR L24 OR L25
- L27 4 S L26 AND L5
- L28 3 DUPLICATE REMOVE L27 (1 DUPLICATE REMOVED)

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	2004/06/15 09:23	USPAT; US-PGPUB; EPO; JPO; DERWENT	protein adj c	8897	L28	BRS	10
2004/06/15 09:24	2004/ 09:24	USPAT; US-PGPUB; EPO; JPO; DERWENT	19 same 24	0	L27	BRS	9
2004/06/15 09:21	2004/ 09:21	USPAT; US-PGPUB; EPO; JPO; DERWENT	21 same 24	0	126	BRS	
2004/06/15 09:23	20 09	USPAT; US-PGPUB; EPO; JPO; DERWENT	20 same 24	12	L25	BRS	7
2004/06/15 09:14	05 20	USPAT; US-PGPUB; EPO; JPO; DERWENT	k251 or lys251	23	L24	BRS	6
2004/06/15 09:12	052	USPAT; US-PGPUB; EPO; JPO; DERWENT	19 same 20	170	L21	BRS	2
2004/06/15 09:12	0 2	USPAT; US-PGPUB; EPO; JPO; DERWENT	(variant or mutant or 333534 fragment or mutat\$3 or substitut\$3 or delet\$3 or addit\$3)	333534 1	L20	BRS	4
2004/06/15 09:10	02	USPAT; US-PGPUB; EPO; JPO; DERWENT	17 or 18	517	L19	BRS	ω
2004/06/15 09:10	0 2	USPAT; US-PGPUB; EPO; JPO; DERWENT	(protein adj c) near human	517	L18	BRS	2
2004/06/15 09:06	00 20	USPAT; US-PGPUB; EPO; JPO; DERWENT	human adj protein adj c	479	L17	BRS	<u> </u>
Time Stamp ment Defi ors	н	DBs	Search Text	Hits	L#	Туре	

	2004/06/15 09:35	US-PA1; US-PGPUB; EPO; JPO; DERWENT	(in adj vivo adj half-life) or (in adj vitro adj half-life)	195	L38	BRS	20
	2004/06/15 09:33	USPAT; US-PGPUB; EPO; JPO; DERWENT	36 same ( 24 or 30)	<b>—</b>	L37	BRS	19
	2004/06/15 09:32	USPAT; US-PGPUB; EPO; JPO; DERWENT	21 same 35	20	L36	BRS	18
	2004/06/15 09:32	USPAT; US-PGPUB; EPO; JPO; DERWENT	32 or 33 or 34	3668	L35	BRS	17
	2004/06/15 09:31	USPAT; US-PGPUB; EPO; JPO; DERWENT	(alpha-1-antitrypsin) or (alpha-1 adj Pl) or (alpha-1 adj proteinase adj inhibitor)	1468	L34	BRS	16
	2004/06/15 09:29	USPAT; US-PGPUB; EPO; JPO; DERWENT	amidolytic adj activity	528	L33	BRS	15
	2004/06/15 09:28	USPAT; US-PGPUB; EPO; JPO; DERWENT	anticoagulant adj activity	1903	L32	BRS	14
	2004/06/15 09:26	USPAT; US-PGPUB; EPO; JPO; DERWENT	28 same 30 same 20	3	L31	BRS	13
	2004/06/15 09:25	USPAT; US-PGPUB; EPO; JPO; DERWENT	(residue adj "251") or (position adj "251")	274	L30	BRS	12
	2004/06/15 09:24	USPAT; US-PGPUB; EPO; JPO; DERWENT	28 same 24	2	L29	BRS	11
Com ment s	Time Stamp ment Defi ors	DBs	Search Text	Hits	# T	Туре	

	Туре	L#	Hits	Search Text	DBs	Time Stamp   Erro   Com   r   Defi   s   nitio   n	Com r Erro ment Defi ors s nitio	Err ors
21	BRS	L39	2	resistance near ( human adj plasma)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:35		
22	BRS	L40	0	21 same (38 or 39)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:36		
23	BRS	L41	318561	318561 (host adj cell) or vector	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:37		
24	BRS	L <i>4</i> 2	78	21 same 41	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:37		!
25	BRS	L <b>43</b>	_	21 same 41 same (24 or 30)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:37		1
26	BRS	144	14	anderson adj kim.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:38		1
27	BRS	L45	53	pedersen adj anders.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:39		
28	BRS	L46	6	freskgaard adj per.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:39		
29	BRS	L47	71	44 or 45 or 46	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:39		1
30	BRS	L48	2	47 and 21	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/15 09:39		

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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
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US-09-997-623-4
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                                                                                             Query Match
Best Local S
Matches 419
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----- Local Similarity
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 419
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Publication No. US20030018175A1
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ORGANISM: Homo
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Pred. No. 3.8e-190;
0; Mismatches 0;
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360 300 300 240

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180 180

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GENERAL INFORMATION:
APPLICANT: Maxygen Holdings
APPLICANT: Maxygen Bps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated pr
FILE REFERENCE: 0219us410 - protein C
CURRENT APPLICATION NUMBER: US/09/997,623
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 09/978,917
PRIOR PILING DATE: 2001-10-17
                                    ANSFLEELRHSSLERECIEBICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
ANSPLEELRHSSLERECTEETCDFEEAKETFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                        100.0%; Score 2324; DB 12;
100.0%; Pred. No. 3.8e-190;
tive 0; Mismatches 0;
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APPLICANT: Grinnell, Brian W
APPLICANT: Grinnell, Brian W
FILE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
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SEQ ID NO 1
LENGTH: 419
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NUMBER OF SEQ ID NOS: 12
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ORGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No. 3.8e-190;
les 419; Conservative 0; Mismatches 0;
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                                                                         SPWQVVLLDSKKKLACGAVL1HPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLD1
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CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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APPLICANI: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
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Local Similarity 100.0%; Pred. No. 3.
Les 419; Conservative 0; Mismatches
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                                                                                               GYHSSREKEAKENRTFYLNFIKIPYVPHNECSEVMSNMYSENMLCAGILGDRQDACEGDS 360
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                     GGPWVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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GGPMVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419
                                                                           GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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US-09-978-917A-2
US-09-978-917A-2
; Sequence 2, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 021948316 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09997623
Publication No. US20030018175A1
GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
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Best Local :
                 Query Match 100.0%; Score 2324; DB 12; Best Local Similarity 100.0%; Pred. No. 4.3e-190;
                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
 Matches 419;
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FRIOR APPLICATION NUMBER: US 09/978,917
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                            FILE REFERENCE: 0219us410 - protein C
CURRENT APPLICATION NUMBER: US/09/997,623
CURRENT FILING DATE: 2001-11-29
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LOCATION: (43)...(461)
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LOCATION: (1)...(42)
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                                                                          LOCATION: (1)...(42)
NAME/KEY: CHAIN
LOCATION: (43)...(461)
                                                                                                                        FEATURE:
NAME/KEY: SIGNAL
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Local Similarity 100.0%;
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RESULT 7
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SEQ ID NO 2
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APPLICANT: Geriltz, Bruce B
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
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CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
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223
                                           181 SPWQVVLLDSKKKLACGAVLTHPSWVLTAAHCKDESKKLLVRLGEYDLRRWEKWELDLDI
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US-10-168-407-2
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CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
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Publication No. US20030207435A1
                    Sequence 3, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
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APPLICANT: Jones, Bryan E
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ORGANISM: Homo sapiens
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APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTMARE: Patentin version 3.1
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US-10-168-407-4
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Publication No. US20030207435A1
GENERAL INFORMATION:
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                                                                                          Matches
                                                                                                                                         Query Match
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ORGANISM: Homo sapiens
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 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                   1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                       1 ANSFLEELRHSSLERBCIEEICDFEEAKBIPONVDDTLAFWSKHVDGDOCLVLPLEHPCA
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Similarity 99.0%;
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                                                                                                      Score 2302; DB 15; ); Pred. No. 2.9e-188;
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Pred. No. 1.3e-188;
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APPLICANT: Huang, Lihua
APPLICANT: Riggin, Ralph M
APPLICANT: Riggin, Ralph M
TITLE OF INVENTION: HUMAN PROTEIN C POLYPEPTIDE
FILE REFERENCE: X-12279
CURRENT APPLICATION NUMBER: US/10/670,628
CURRENT FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
SOFTWARE: Patentin version 3.1
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US-10-670-628-2
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Best Local Similarity
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ORGANISM: Artificial Sequence
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                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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; TYPE: PRT; ORGANISM: Homo sapiens US-10-168-407-5
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APPLICANT: Geriltz, Bruce E
APPLICANT: JONES, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
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Publication No. US20030207435A1
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Best Local Similarity 98.8%;
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CURRENT FILING DATE: 2002-11-04
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                             GYHSSREKEAKRNRTFVLNEIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQD ACEGDS
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; Pred. No. 6.3e-188;
2; Mismatches 3;
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RESULT 13
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US2003002354A1
; GENERAL INFORMATION:
   APPLICANT: Gerlitz, Bruce E
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan B
; APPLICANT: Jones, Bryan B
; APPLICANT: Jones, Bryan B
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT APPLICATION NUMBER: 60/181948
; PRIOR APPLICATION NUMBER: 60/181949
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
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US-10-168-407-6
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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Best Local Similarity 98.8%;
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Publication No. US20030207435A1
GENERAL INFORMATION:
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                                                                                                                   Matches 413;
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Best Local
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CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
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TYPE: PRT
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Similarity 98.6%;
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SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                        ANSFLEELROGSLERECIEET CDFEEAKETFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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Pred. No. 9.4e-188;
                                                                                                                              Score 2294; DB 15; Length 419; Pred. No. 1.4e-187;
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CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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US-10-182-263-3
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Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
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LENGTH: 419
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TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
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Pred. No. 3.1e-187;
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US-10-182-263-4
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Publication No. US20030022354A1
GENERAL INFORMATION:
                                                                                                                                    Sequence 4, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
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Best Local :
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
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                     APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
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CURRENT APPLICATION NUMBER: US/10/182,263
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ORGANISM: Homo sapiens
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US-10-182-263-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10406031; Publication No. US20040043017A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-406-031-27
                                                                                                US-10-406-031-27
                                                                                                                                                                                  ; SEQ ID NO 27
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PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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  Query Match 34.8%; Score 809; DB 12; Best Local Similarity 35.7%; Pred. No. 1.5e-60; Matches 163; Conservative 87; Mismatches 151;
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                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: AU PS1483
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Masci, Paul Pantaleone
APPLICANT: De Jersey, John
APPLICANT: Lavin, Martin
TITLE OF INVENTION: PROTHEMBIN ACTIVATING PROTEIN
PILE REFERENCE: 15685-002001
CURRENT APPLICATION NUMBER: US/10/406,031
CURRENT FILING DATE: 2003-044-02
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TYPE: PRT
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PRIOR FILING DATE: 2003-03-07
                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                             TYPE: PRT
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Local Similarity 98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SPWQVVLLDSKKKSACGAVLIHPSWVLTAAHCMDESKKILVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKKMBKKRSHLKRDTEDQEDQVFPRLIKGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPMVASFHGTWPLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYHSSREKEAKRNRTFVLNPIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 6.7e-187;
3; Mismatches 4;
         151;
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Length 488;

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US-10-348-504-44
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Publication No. US20030138914A1
GENERAL INFORMATION:
                        APPLICATION NUMBER: WO PCT/AT98/00046 FILING DATE: 27-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/348,504
FILING DATE: 29-Jan-2003
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Factor X Deletion Mutants and Analogues Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Himmelspach, Michele
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANS FLEELRHSS LERECIEEICD FEEAKEIF QNVDDTLAFWSKHVDGDQCLVLPLEHPCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPITFRMNVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 209
                                                                                                  APPLICATION NUMBER: US/09/367,777
FILING DATE: 10-No. US20030138914A1-1999
APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfleiderer, Michaei
Falkner, Falko-Guenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eibl, Johann
Dorner, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
US-10-407-123-27
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/10407123
Publication No. US20030181381A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-000900US
TELECOMPUNICAȚION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                  a Modified Protease Cleavage Site NUMBER OF SEQUENCES: 122
                                                                                                                                                                                                                                         TITLE OF INVENTION: Factor X Analogues With
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Himmelspach, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 TPITFRMNVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECFWQALLINEENEGFCGGTILSEF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED-------QVD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 -- CONOGRCKDGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEONSVVCSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SICCGHGTCIDGIGSESCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGES 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
        COUNTRY: USA
ZIP: 94111-3834
                                                                               CITY: San Francisco
                                                         STATE: CA
                                                                                                                                                                                                                                                                                                                                           Schlokat,
                                                                                                                                                                                                                                                                                    Fisch, Andreas
                                                                                                                                                                                                                                                                                                             Dorner, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.6%; Score 803; DB 14; 35.4%; Pred. No. 4.7e-60;
                                                                                                                                                                                                                                                                    Johann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
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                                                                                                                                                                                                                                                                                                                                                  205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVPVHPNYSKSTTONDIALLHLA 264
443
                                                                                                383 PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGES 442
                                              384 CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                               324 PVVPHNECSEVMSNYVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
                                                                                                                                                                                                                                               265 QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSP----- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLEELRHSSLERECIBEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 34.6%; Score 803; DB 14; Similarity 35.4%; Pred. No. 4.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. US20030181381A1-1999
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-Apr-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 479
                                                                                                                                                                                                TPITFRMNVAPACLPERDWABSTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 382
                                                                                                                                                                                                                                                                                                YILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLK 329
                                                                                                                                                                                                                                                                                                                                                                                                 PTENPFOLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --CONQGKCKDGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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RESULT 21 US-09-782-587B-3

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; ORGANISM: Homo sapiens
US-09-782-587B-3
                                                                                                                                                                                                                                                   RESULT 22
US-10-383-898-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: PatentIn Ver. 2.1 SEQ ID NO 3
                                            GENERAL INFORMATION:
APPLICANT: EMOTY University
ITITLE OF INVENTION: Curcuminoid-protein conjugates
FILE REFERENCE: E056 1060.1
CURRENT APPLICATION NUMBER: US/10/383,898
CURRENT FILING DATE: 2003-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.7%; Score 783; DB 10; Best Local Similarity 38.8%; Pred. No. 1.9e-58; Matches 164; Conservative 76; Mismatches 147)
                                                                                                                                                                                            Sequence 1, Application US/10383898
Publication No. US20040009914A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/184,036
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/241,916
PRIOR FILING DATE: 2000-10-18
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APPLICANT: BORNAES, CLAUS
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 19
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 DRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 LDLDIKEVFYHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                               335 GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 QSRRVAQVIIPSTYVPGTTNHDIALLRIHQPVVLTDHVVPLCLPERTFSERTLAPV-RPS
                                                                                                                                                                                                                                                                                                                                                   395 PRP 397
                                                                                                                                                                                                                                                                                                                                                                                                     411 EAP 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVSGWGQLLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GECPWOVILLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE 220
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                                       CURRENT PPLICATION NUMBER: US/10/263,205B
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 08/464,029
PRIOR TILING DATE: 1995-06-05
PRIOR PPLICATION NUMBER: 08/327,690
PRIOR PILING DATE: 1994-10-24
PRIOR PPLICATION NUMBER: PCT/US94/05779
PRIOR PPLICATION NUMBER: PCT/US94/05779
PRIOR APPLICATION NUMBER: 08/065,725
PRIOR APPLICATION NUMBER: PCT/US92/01636
PRIOR PILING DATE: 1993-05-21
PRIOR APPLICATION NUMBER: PCT/US92/01636
PRIOR APPLICATION NUMBER: PCT/US92/01636
PRIOR APPLICATION NUMBER: PCT/US92/01636
PRIOR APPLICATION NUMBER: PCT/US92/01636
PRIOR APPLICATION NUMBER: 07/662,920
PRIOR APPLICATION NUMBER: 07/662,920
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US-10-263-205B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10263205B Publication No. US2004008749BA1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 164; Conservative 76; Mismatches 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BERKNER, Kathleen L. APPLICANT: PETERSEN, Lars APPLICANT: HART, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MODIFIED FACTOR VII FILE REFERENCE: 13952N-8-5-1
NUMBER
                         PRIOR FILING DATE: 1991-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CHAIN
LOCATION: (1)..(406)
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OF SEQ ID NOS: 5
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BREGENGAARD, Claus
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PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR PILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10411037; Publication No. US20040043446A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2 SEQ ID NO 2
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APPLICANT:
                                                                                                                                                                                                                                                                                        APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A
FILE REFERENCE: 040863-01-5082
CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT FILING DATE: 2003-04-09
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TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 38.8%; Pred. No. 1.9e-58;
ses 164; Conservative 76; Mismatches 147;
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Hakes, David
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Zopf, David
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Bowe, Caryn
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US-10-382-248-34
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; TYPE: PRT; CRGANISM: Homo sapiens US-10-382-248-34
                                                                                                                                                   PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/361,974
PRIOR TRILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR FILING DATE: 2002-03-19
PRIOR PRIOR PRIOR DATE: 2002-08-06
PRIOR FILING DATE: 2002-08-06
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/10382248 Publication No. US20040058347A1 GENERAL INFORMATION:
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                                                                                          SEQ ID NO 34
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/382,248
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/366,928
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-568C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                             SOFTWARE: CuraSeqList version 0.1
                                                                                                                                     NUMBER OF SEQ ID NOS: 82
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APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THI
FILE OF INVENTION: METHODS
FILE REFERENCE: 040853-01-5053
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-0-10
PRIOR PILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/349,792
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
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US-10-411-026-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Publication No. US20040063911A1
                                                                     PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Neose Technologies,
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
ORGANISM: Homo sapiens
                          LENGTH: 444
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 LVSGWGQLLDRGATA----LELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSD 372
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Hakes, David
Chen, Xi
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US-10-411-026-8
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10410962 Publication No. US20040077836A1
                                                                        PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR TILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF FILE REFERENCE: 040683-01-5054 CURRENT APPLICATION NUMBER: US/10/410,962 CURRENT FILING DATE: 2003-04-09 PRIOR APPLICATION NUMBER: US 60/328,523 PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/387,292 PRIOR FILING DATE: 2002-06-07
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Bowe, Caryn
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Hakes, David
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US-10-410-962-8
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US-10-411-049-8
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                             PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR RILING DATE: 2002-06-25
PRIOR RILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON TITLE OF INVENTION: ALPHA FILE REFERENCE: 040853-01-5055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRICE APPLICATION NUMBER: US 60/328,523
                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
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          APPLICATION NUMBER: US FILING DATE: 2002-08-28
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Zopf, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, Xi
Bowe, Caryn
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US-10-263-205B-3
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SEQ ID NO 8
LENGTH: 444
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APPLICANT: BERKIER, Kathleen L.
APPLICANT: PETERSEN, Lars
APPLICANT: HART, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10263205B Publication No. US20040087498A1
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                                                               PRIOR FILING DATE: 1994-05-23
PRIOR APPLICATION NUMBER: 08/065,725
PRIOR FILING DATE: 1993-05-21
PRIOR APPLICATION NUMBER: PCT/US92/01636
PRIOR FILING DATE: 1991-02-28
PRIOR APPLICATION NUMBER: 07/662,920
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 13952N-8-5-1
CURRENT APPLICATION NUMBER: US/10/263,205B
CURRENT FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MODIFIED FACTOR VII
                                                                                                                                                                                                       PRIOR FILING DATE: 1994-10-24
PRIOR APPLICATION NUMBER: PCT/US94/05779
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/464,029 PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/327,690
                                              PRIOR FILING DATE: 1991-02-28
                        NUMBER OF SEQ ID NOS:
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BREGENGAARD, Claus
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US-10-017-122-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10017122
Publication No. US20030087244A1
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SBQ ID NO 2
LENGTH: 466
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                                                                                                                                                             Matches
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 66/327,487
PRIOR FILING DATE: 2001-10-09
RUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: McCarthy, Jeanette
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-007
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 LYTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM----SNMVSENMLCAGILG 350
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                                                                                                                                                             164;
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61 SICCGHGTCIDGIGSFSCDCRSGMEGRFCQ-REVSFLNCSIDNGGCTHYCLEEVGWRR-C
                                                                     61 ANAFLEBURPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC-----AS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
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                                                                                                             ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                  Conservative
                                                                                                                                                           33.7%; Score 783; DB 14; Length 466; 38.8%; Pred. No. 2.3e-58; ative 76; Mismatches 147; Indels 3
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RESULT 31
US-10-375-741-14
/ Sequence 14, Application US/10375741
/ Publication No. US20030232753A1
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Best Local Similarity
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TITLE OF INVENTION: TISSUE FACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
FILE REFERENCE: 4001.001999
CURRENT APPLICATION NUMBER: US/10/375,741
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APPLICANT: King, Steven W
APPLICANT: Gao, Boning
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NUMBER OF SEQ ID NOS: 27
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PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 60/035,920
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PRIOR APPLICATION NUMBER: 60/042,427
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TYPE: PRT
ORGANISM: Homo sapiens
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173 RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA------SKPQGRIVGGKVCPK 221
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                                                SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTBDQEDQVDPRLIDGKWTRR 178
                                                                                                SPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC
                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEBVGWRR-C
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PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Publication No. US20040043017A1
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PRIOR PILING DATE: 2003-03-07
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CURRENT APPLICATION NUMBER: US/10/406,031
CURRENT FILING DATE: 2003-04-02
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRPCQREVSPLNCSLDNGGCTHYCLEEVGWRRCSC 120
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          PTADFANQVLMKQ-DFGIISGFG--RIFEKGPKSN---TLKVLKVPYVDRHTCMVSSESP 384
                                                                                                                                                           EKWELDLDIKEVFVHPN-----
                                                     PDSGLAERELNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPYVPHNECSEVMSNM 338
                                                                                                        ETGHL-LSVDKIYVHKKFVPPKKGYKFYEKFDLVSYDYDIAIIQMKTPIQFSENVVPACL 330
                                                                                                                                                              -YSK---STIDNDIALLHLAQPATLSQTIVPICL 278
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Publication No. US20040043017A1
GENERAL INFORMATION:
APPLICANT: Masci, Paul Pantaleone
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PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGIH: 467
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CURRENT APPLICATION NUMBER: US/10/406,031
CURRENT FILING DATE: 2003-04-02
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APPLICANT: Lavin, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 33.6%; Score 782; DB 12; Local Similarity 37.7%; Pred. No. 2.8e-58;
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  445
                                         399 YLDWIHGHIRDK 410
                                                                                 385 ITPTMFCAGYDTLPRDACQGDSGGPHITAYRDTHFITGIVSWGEGCAQTGKYGVYTKVSK 444
                                                                                                                         339 VSENMLCAGILGDRODACEGDSGGPMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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FILWIKRIMRQK 456
                                                                                                                                                                                                        PDSGLAERELNOAGOETLYTGWGYHSSREKEAKKNRTFVLNFIKIPVVPHNECSEVMSNM 338
                                                                                                                                                                                                                                                      NPGRL-LSVDKIYVHQKFVPPKKGYEFYEKFDLVSYDYDIAILQMKTPIQFSENVVPACL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTADFANQVLMKQ-DFGIVSGFGRIFEKGFQSK-----TLKVLKVPYVDRHTCMLSSESP 384
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CURRENT APPLICATION NUMBER: US/10/406,031
CURRENT FILING DATE: 2003-04-02
FRIOR APPLICATION NUMBER: AU 2003901033
PRIOR TILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: AU PS1483
PRIOR FILING DATE: 2002-04-03
NUMBER: OF SEQ ID NOS: 51
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AESYRLGDDGHSCVAEGDFSCGRNIKARNKREASLPDFVQSQNATLLKKSDNPSPDIRII 211
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                                                                                    385 PRDACQGDSGGPHITAYRDTHFITGIISWGEGCAKKGKYGVYTKVSNFIPWIKAVMRKHQ 444
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445 PSTES
                                        412 APQKS 416
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                                                                                                                            RODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKE 411
                                                                                                                                                                            -DFGIISGFGHTRSGGQTSN-----TLKVVTIPYVDRHTCMLSSDFRITPNMFCAGYDTL 384
                                                                                                                                                                                                                 GQETLVTCWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGD 351
                                                                                                                                                                                                                                                                ETRHĹ-ĹSVDKAYVHTKFVLATYDYDÍAIIQÍKTÞIQFSENVVÞACLFTAÐFÁNQVLMKQ 330
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RESULT 35
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Publication No. US20040009550A1
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                       FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
                                                                                                                                                                            APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
PRIOR APPLICATION NUMBER: EP 02077060.8 PRIOR FILING DATE: 2002-05-24 NUMBER OF SEQ ID NOS: 309
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RESULT 34 US-10-406-031-11

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                                                                                                                                     ; ORGANISM: Pseudonaja textilis US-10-406-031-2
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Matches 162; Conservative
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                              Query Match
33.4%; Score 777; DB 12;
Best Local Similarity 37.5%; Pred. No. 7.5e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 15685-002001
CURRENT APPLICATION NUMBER: US/10/406,031
CURRENT FILING DATE: 2003-04-02
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: AU PS1483
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lavin, Martin
      77; Mismatches 155;
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CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: AU 2003901033
PRIOR TILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: AU PS1483
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/10406031 Fublication No. US20040043017A1
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TITLE OF INVENTION: PROTHROMBIN ACTIVATING
FILE REFERENCE: 15685-002001
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                                                                         121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQV------DPRLI 171
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                                                                                                                                                                                                                                                                                                                         41 SNSLFEETRPGNIERECTEEKCSKEEAREVFEDNEKTETFWNVYVDGDQCSSNP----- 94
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AESYRLGVDGHSCVAEGDFSCGRNIKARNKREASIPDFVQSQKATLLKKSDNPSPDIRIV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.4%; Score 775.5; DB 12; Length 455; ilarity 37.0%; Pred. NO. 9.7e-58; Conservative 79; Mismatches 151; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 151; Indels 37;
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40	Db 331 DFA-KEYLMKQDSGIVSGFGRTQSIGYTSNILKVITVPYVDRHTCMLSS 378
Db 4	QY 282 GLAERELNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVM 335
Qy	Db 272 ETRRL-LSVDKIYVHKKFVPPNSYYQNIDREAYDYDIAIIRMKTFIQESENVVPACLPTA 330
Matches 1	VHPNYSKSTTDNDIALLHLAQPATLSQT
Query Mato Best Local	
; SEC US-10-712-33	172 TICKMTBRGTNSPWOVVI.I.DSKKKI.ACGAVI.IHPSWVI.TAAHCWDESKKI.I.VRLGEVDI.RRW
·. ·· ··	OY 121 APGYKLGDDLLQCHPAVKEPCGRPWKKMEKKRSHLKRDTEDQEDQVDRRLI 171
; ;	FCKRVQSETQCSC
 	— C
; ; TEL	Qy 1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 :
; ; ATT	Query Match  32.6%; Score 758.5; DB 12; Length 453;  Best Local Similarity 36.7%; Pred. No. 2.7e-56;  Matches 157; Conservative 75; Mismatches 149; Indels 47; Gaps 8;
** ** **	; TYPE: PRT ; ORGANISM: No. US20040043017Alechis scutatus US-10-406-031-14
	SEQ for
	; PRIOR APPLICATION NUMBER: AU PS1483 ; PRIOR FILING DATE: 2002-04-03 ; NUMBER OF SEQ ID NOS: 51
*. *. *.	; CURRENT FILING DATE: 2003-04-02 PRIOR APPLICATION NUMBER: AU 2003901033 PRIOR FILING DATE: 2003-03-07
; PRI	N-1 177
; curi	; APPLICANT: De GEREY, COMI ; APPLICANT: LAVID, MARCIN ; TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
. ~ ~	GENERAL INFORMATION: APPLICANT: Masci, Paul Pantaleone
COMI	RESULT 38 US-10-406-031-14 IS-quence 14, Application US/10406031 Publication No. US20040043017A1
	Db 445 IPWI 448
CORF	Qy 400 LDWI 403
; TITI	385
; GENERAL I ; APPI	340
RESULT 39 US-10-712-332	Qy Z8U DSGLAERELNQASQETLYTIGWGITISSKENEALAUKIKTE VLNE LALEVYETHELSEVENEW 333
Db 439	272 ETRRL-LSVDKIYVHTKEVPPNYYYVHQNEDRVAXDYDIAIIRMKTPIQESENVVPACLP
	OY 232 EKWELDLDIXEVFVHPNYSKSTTDNDIALIHLAQPATLSQTIVPICLE 279
Db 379	Db 212 NGMDCKLGECPWQAVLINEKGEVFCGGTILSPIHVLTAAHCINQTKSVSVIVGEIDISRK 271
Qy 336	Qy 172 DGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRW 231

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APPLICATION UNMBER: US/10/712,332
FILING DATE: 13-Nov-2003
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/09/671,346
FILING DATE: 27-Sep-2000
APPLICATION UNMBER: US 07/578,646
FILING DATE: 199-09-04
APPLICATION UNMBER: US 07/808,329
FILING DATE: 199-101-16
APPLICATION UNMBER: US 08/249,777
FILING DATE: 1994-05-26
APPLICATION UNMBER: US 08/268,003
FILING DATE: 1994-06-29
APPLICATION UNMBER: US 08/469,301
FILING DATE: 1994-06-29
APPLICATION UNMBER: US 09/469,301
FILING DATE: 1995-06-06
APPLICATION UNMBER: US 09/016,403
FILING DATE: 1998-01-30
APPLICATION UNMBER: US 09/362,207
FILING DATE: 1998-01-30
APPLICATION UNMBER: US 09/362,207
FILING DATE: 1999-07-28
ATTORNEY/AGENT INFORMATION:
NAME: MICHAEL S. TUSCAI, Ph.D.
REFERENCE/DOCKET NUMBER: 44,481-5002-15-US
TELEPHONE: (202) 739-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 SNMVSENMLCAGILGDRQDACEGDSGGPMVASEHGTWELVGLVSWGBGCGLILHNYGVYTK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sinha, Uma
Sinha, Uma
TILE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
MBER OF SEQUENCES: 11
RRESSPONDENCE ADDRESS:
ADDRESSE: Morgan, Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 VSNFIPWI 446
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                                                                                                                                                                                                                                                                                                                     QUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                            41 ANSFLXXMKKGHLXRXCMXXTCSYXXARXVFXDSDKTNXFWNKYKDGDQCETSP----- 94
                                                                                                                                                                    ch 32.3%; Score 749.5; DB 12; Length 437; L Similarity 35.6%; Pred. No. 1.5e-55; 150; Conservative 82; Mismatches 154; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
PLICANT: Wolf, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 VSRYLDWI 403
                                                                                           1 ANSFLEELRHSSLERBCIBEICDEBEAXBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                       NAME/KHY: Modified-site
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 39
OTHER INFORMATION: /note= "Xaa = gamma-carboxy glutamic
acid."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 739-3001
                                                                                                                                                                                   154; Indels 35; Gaps
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RESULT 40
US-10-712-332-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis NUMBER OF SEQUENCES: 11
REFERENCE/DOCKET NUMBER: 44481-5002-15-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 739-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wolf, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 WGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVVIKHNRFTKETYDEDIAVLRLKTPITFRMNVAPACLPERDWAESTL--MTQKTGIVSG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET-LVTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPWQALLINEENEGPCGGTILSEFYILTAAHCLYQAKRPKVRVGDRNTEQEEGGEAVHEV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/712,332 FILING DATE: 13-Nov-2003
                                                                                                                                                                                                 APPLICATION NUMBER: US 08/469,301 FILING DATE: 1995-06-06 APPLICATION NUMBER: US 09/016,403
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/671,346 FILING DATE: 27-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1111 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Morgan, Lewis & Bockius LLP
                                                              NAME: Michael S. Tuscan, Ph.D. REGISTRATION NUMBER: 43,210
                                                                                                                                                        FILING DATE: 1998-01-30
APPLICATION NUMBER: US 09/362,207
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/268,003 FILING DATE: 1994-06-29
                                                                                                                                                                                                                                                                                                                FILING DATE: 1994-05-26
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1990-09-04
APPLICATION NUMBER: US 07/808,329
                                                                                                                                     FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/249,777
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1991-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/578,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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US-10-712-332-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan,
                             FILING DATE: 13-NOV-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/671,346
FILING DATE: 27-6ep-2000
APPLICATION NUMBER: US 07/578,646
                                                                                                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wolf, David L. Sinha, Uma
                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/712,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ANSFLXXMKKGHLXRXCMXXTCSYXXARXVFXDSDKTNXFWNKYKDGDQCETSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 39
OTHER INFORMATION: /note= "Xaa = gamma-carboxy glutamic acid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 6, 7, 14, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARKGKYGIYIKVTAFLKWIDRSMKTRGLPKAKSHAP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPITFRMNVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKWLEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --CONOGRCKXGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEONSVVCSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 739-3001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 209
                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                              STREET: 1111 Pennsylvania Avenue, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
           FILING DATE: 1990-09-04
                                                                                                                                                                                                                                                                                                  20004
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33.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 746; DB 12;
Pred. No. 3.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 488;
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                                                                                                                                                   RESULT 42
US-10-038-854-94
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                                                                             Sequence 94, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
              APPLICANT: Spytek, APPLICANT: Li, Li
APPLICANT: Wolenc,
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Michael S. Tuscan, Ph.D.
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44481-5002-15-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 739-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-07-28 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 ARGYTLADNGKACI PTGPYPCGK--QTLERRKR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                         368 AGGEHVTREKDTYEVTGIVSWGEGCAKKGKYGIYTKVTAFLKWIDRSMKTRGLEKAKSHA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                  313 FGRTHEKGROSTR-----LKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 WGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 EVVIKHNRFTKETYDFNIAVLRIKTPITFRMNVAPAČLPERDWAESTL--MTQKTGIVSG 312
                                                                                                                                                                                                                                                  428 P 428
                                                                                                                                                                                                                                                                                             419 P 419
                                                                                                                                                                                                                                                                                                                                                                                       360 SGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ANSFLXXMKKGHLXRXCMXXTCSYXXARXVFXDSDKTNXFWNKYKDGDQCETSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA 60
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FILING DATE: 1995-06-06
APPLICATION NUMBER: US 09/016,403
FILING DATE: 1998-01-30
APPLICATION NUMBER: US 09/362,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 39
OTHER INFORMATION: /note= "Xaa = gamma-carboxy glutamic acid."
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APPLICATION NUMBER: US 08/268,003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEVEVHANSKSTIDNOIALLALAGPATLSQTIVPICLPDSGLAFRELNDAGQET-LVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPWQALLINEENEGFCGGTILSETYILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --CQNQGKCKKGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 739-3001
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Vernet,
                                                                 Kimberly A
                     Adam R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RIVGGQECKDGE 194
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LENGTH: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
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; TYPE: PRT; ORGANISM: Pan troglodytes US-10-038-854-94
                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.8%; Score 740; DB 16; Length 461; Best Local Similarity 35.6%; Pred. No. 1.1e-54; Matches 151; Conservative 71; Mismatches 156; Indels 4
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CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
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APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/259,785 PRIOR FILING DATE: 2001-01-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/284,447
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                                                       161 YRLAENQKSCEPAVPFPCGRVSVSQTSKLTRAETVFPDVDYVNSTEAETILDNITQSTQS 220
                                                                                                                                                             104 NGGSCKDDINSYECWCPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG
168 ----PRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRL 223
                                                                                                   124 YKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKR-----DTEDQEDQVD------
                                                                                                                                                                                                         65 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
                                                                                                                                                                                                                                                                   52 LEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVDGDQCESNP-----CL 103
                                                                                                                                                                                                                                                                                                                  5 LEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ellerman, Karen
Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burgess, Catherine
Edinger, Shlomit R
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Gusev, Vladimir Y
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Kekuda, Ramesh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xiaojia S
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RESULT 43
US-10-038-854-96
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Publication No. US20040022781A1
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                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
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                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/258,928
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IITLE OP INVENTION: Proteins and Nucleic Acids Encoding Same
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APPLICATION NUMBER: 60/283,889 FILING DATE: 2001-04-13 APPLICATION NUMBER: 60/284,447
                                                                                                                 APPLICATION NUMBER: 60/279,833
                                                                                                                                                                               FILING DATE:
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APPLICATION NUMBER: 60/269,814
                                                       APPLICATION NUMBER: 60/279,863 FILING DATE: 2001-03-29
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                                                                                                                                                      APPLICATION NUMBER: 60/279,832
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Gunther, Erik
Smithson, Glennda
Millet, Isabelle
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Rastelli,
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Edinger, Shlomit R
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Gusev, Vladimir Y
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Shimkets, Richard A
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li, Luca
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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 411
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 96
LENGTH: 456
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PRIOR APPLICATION NUMBER: 60/286,683
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                                                           Gusev, Vladimir 1
Gangolli, Esha A
Guo, Xiaojia S
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Shimkets, Richard A
Tchernev, Velizar
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Liu, X
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      Casman,
                      Shenoy, Suresh G
Rastelli, Luca
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Kekuda, Ramesh
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        Stacie
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                                                                                Esha A
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SOUTWARE: Patentin Ver. 2.1
SEQ ID NO 95
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PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
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PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
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PRIOR FILING DATE: 2001-01-04
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MacDougall, John R
VENTION: Proteins and Nucleic Acids Encoding Same
YNNMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRY
                                              SENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRY
                                                                                         EYTNIFLKFG--SGYVSGWGRVFHKGRS-----ALVLQYLRVPLVDRATCLRSTKFTI
                                                                                                                                     GLAERELNQAGQETLYTGWG--YHSSREKEAKRNRTFYLNFIKIPVYPHNBCSEVMSNMV
                                                                                                                                                                                   GEHNIEETEHTEQKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADK 334
                                                                                                                                                                                                                       GEYDLRRWEKWELDLDIKEVFVHFNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPDS 281
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Gunther, Erik
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US-10-132-829-5
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                                                             GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 150;
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CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/212,902
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TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of
FILE REFERENCE: UOFW-1-17396
                                                                                                                         Sequence 5, Application US/10132829 Publication No. US20030044982A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VJ TITLE OF INVENTION: with vesicle vector FILE REFERENCE: 6627-PA1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homosapien
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PRIOR APPLICATION NUMBER: US 60/261,751
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,751
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin version 3.1
SEQ ID NO 6
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CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,314
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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                                                                                                                                                                        APPLICANT: ROLLAND, Alain
TITLE OF INVENTION: NUCLEIC ACID FORMULATIONS FOR GENE DELIVERY AND METHODS OF USE
FILE REFERENCE: 54964.8033.US01
CURRENT APPLICATION NUMBER: US/10/234,406
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US 60/187,236
PRIOR FILING DATE: 2000-03-03
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CRGANISM: Homo
LENGTH: 461
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                                                                                                                                                                                                                                                                                                                                                                                        MACLAUGHLIN,
                                                                                                                                                                                                                                                                                                                                          SMITH, Louis C. NICOL, François
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                                                                                                                                              NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10234406 Publication No. US20030109478A1
                                                                                                                                                                                                              APPLICANT: MITH, LOUIS C.
APPLICANT: MITH, LOUIS C.
APPLICANT: MICH, François
APPLICANT: NICOL, François
APPLICANT: NICOL, François
APPLICANT: NICOLAND, Alain
TITLE OF INVENTION: NUCLEIC ACID FORMULATIONS FOR GENE DELIVERY AND METHODS OF USE
FILE REFERENCE: 54964.8303.US01
CURRENT APPLICATION UNMBER: US/10/234,406
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION UNMBER: US 60/187,236
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FEWEL, Jason G
APPLICANT: MACLAUGHLIN, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Expression plasmid pru0945 having natural sequence encoding human OTHER INFORMATION: coagulation factor IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Expression plasmid pFN1645 having codon optimized sequence encod OTHER INFORMATION: ng for human coagulation factor IX (786) ... (2171).
                                                      FEATURE:
                                                                     ORGANISM: Artificial Sequence
                                                                                                  TYPE: PRT
                                                                                                                      ENGTH: 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340
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Similarity 35.4%; Pr
50; Conservative 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTNIFLKFG--SGYVSGWGRVFHKGRS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAERELNQAGQETLVTGWG--YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMV 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENDFTRVVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVA 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEHNIEETEHTECKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fiona
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Pred. No. 2.4e-54;
72; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ALVLQYLRVPLVDRATCLRSTKFTI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 46;
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US-10-234-406-8
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US-10-133-907-5
                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo
US-10-133-907-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10133907 Publication No. US20030195223A1
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chien, Kenneth R APPLICANT: Hoshijima, Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/286,314 PRIOR FILING DATE: 2001-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/133,907 CURRENT FILING DATE: 2002-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VITITLE OF INVENTION: with vesicle vector FILE REFERENCE: 6627-PA1170
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 461
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                 104 NGGSCKDDINSYECWÖPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG
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                                                          65 GHGTCIDGIGSESCDCRSGWEGRECOREVSELNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
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                                                                                                                                 LEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCASLCC 64
                                                                                                         LEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVDGDQCESNP-----CL 103
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                   31.7%; Score 736; DB 14; Length 461; 35.4%; Pred. No. 2.4e-54; ative 72; Mismatches 156; Indels 4
                                                                                                                                                                                                 72;
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                                                                                                                                                                                                        Indels 46;
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US-10-038-854-92
; Sequence 92, Application US/10038854
; Publication No. US2004002278181
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                                                          FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR REPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR APPLICATION NUMBER: 60/259,814
PRIOR REPLICATION NUMBER: 60/279,832
PRIOR REPLICATION NUMBER: 60/279,832
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR APPLICATION NUMBER: 60/279,832
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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  PRIOR
                                            R FILING DATE: 2001-02-20
R APPLICATION NUMBER: 60/279,832
R FILING DATE: 2001-03-29
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APPLICATION NUMBER: 60/279,833 FILING DATE: 2001-03-29
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Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
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Gunther, Erik
Smithson, Glennda
Millet, Isabelle
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Shimkets, Richard F
Tchernev, Velizar
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Bisen, Andrew J
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Boldog, Ferenc
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Edinger, Shlomit R
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Gusev, Vladimir Y
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PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 93, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
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                                                                                                                Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
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                                                                                                                                                                                                                                                                                                        Vernet,
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                                                                                     Gorman, Linda
                                                                                                                                                                                                                                             Liu, Xiaohong
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                                                                                                                                                                                                                                                                                 Andrew J
                                                                                                                                                                                                                                                                                                                  Corine
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SEQ ID NO 93
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PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
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CURRENT FILING DATE: 2003-01-22
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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PRIOR FILING DATE: 2001-01-04
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PRIOR FILING DATE: 2001-03-29
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      340 EYTNIFİKFG--SGYVSGWGRVFHKGRS----ALVLQYLRVFLVDRATCLRSTKETI 390
                                                              282 GLAEREĻNQAGQETLŲTGWG--YHSSREKEAKRNRTFVĻNFIKIPVVPHNECSEVMSNMV 339
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Ellerman, Karen
Gunther, Erik
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                                                                                                                                                                                                                                                   FNDFTRVVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTÄAHCVETGVKITVVA 279
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; ORGANISM: Homo sapiens
US-10-239-498A-5
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LENGTH: 461
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CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: PCT/EP01/03220
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Schroder, Carola
APPLICANT: Lehnerer, Michael
TITLE OF INVENTION: Production of Recombinant Blood Clotting Factors
TITLE OF INVENTION: Human Cell Lines
FILE REFERENCE: 80977.0001
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APPLICANT: Horster, Andrea
APPLICANT: Schroder, Carola
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451
                                        400 LDWI 403
                                                                                         391 YNNMFCAGFHEGGRDSCOGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRY 450
                                                                                                                                  340 SENMLCAGILGDRODACEGDSGGEMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRY 399
                                                                                                                                                                                                                           282 GLAERELNQAGQETLYTGWG--YHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMV 339
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                                                                                                                                                                                                                                                                                                                      GEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPDS 281
VNWI 454
                                                                                                                                                                                  EYTNIFLKFG--SGYVSGWGRVFHKGRS--
                                                                                                                                                                                    ---ALVLQYLRVPLVDRATCLRSTKFTI
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EARLIER FILING DATE: 1997-07-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                        168 ----PRLIDGKMTRRGDSPWQVVLLDSKKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRL 223
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                                            400 LDWI 403
                                                                                         345 YNNMFCAGFHEGGRDSCOGDSGGPHVTEVEGTSFLTGIISWGEECANKGKYGIYTKVSRY 404
                                                                                                                                    340 SENMICAGILGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRY 399
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405 VNWI 408
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                                                                                                                                                                                   EYTNIFLKFG--SGYVSGWGRVFHKGRS-----ALVLQYLRVFLVDRATCLASTKFTI 344
                                                                                                                                                                                                                             GLAERELNOAGOETLYTGWG--YHSSREKEAKRNRTEYLNFIKIPYVPHNECSEVMSNMV 339
                                                                                                                                                                                                                                                                               GEHNIEETEHTEOKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADK 293
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US-09-782-587B-1
US-09-782-587B-1
US-09-782-587B-1
Sequence 1, Application US/09782587B
Publication No. US20030096338A1
GENERAL INFORMATION:
APPLICANT: PEDERSON, ANDERS H.
APPLICANT: DORNAES, CLAUS
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
FILE REFERENCE: 31-001100US
CURRENT APPLICATION NUMBER: US/09/782,587B
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: W3/09/782,587B
PRIOR APPLICATION NUMBER: W3/09/782,587B
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-22
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RESULT 53 US-09-118-748-2

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PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 19
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OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic
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OTHER INFORMATION: Gamma carboxyglutamic
NAME/KEY: MOD RES
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OTHER INFORMATION: Gamma carboxyglutamic NAME/KEY: MOD_RES
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OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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ORGANISM: Homo sapiens
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                                                                                                                                                                  335 GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE 394
                                                                                                                                                                                                                                                                                     296 LYTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM----SNMVSENMLCAGILG 350
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                                                                                   395 PRP
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                                                                                                                                                                                                                                                 LVSGWGQLLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSD 334
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Sequence 1, Application US/10617500 Publication No. US20040072755A1

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                                                                                                                                                            RESULT 56
US-10-109-498-1
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APPLICANT: Stennicke, Henning R
APPLICANT: Bjorn, Soren E
APPLICANT: Petersen, Lars C
TITLE OF INVENTION: TF Antagonist
FILE REFERENCE: 6510.200-US
GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: PURENTION: Coagulation Factor VII Derivatives
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286.200-US
CURRENT APPLICATION NUMBER: US/10/109,498
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PRIOR APPLICATION NUMBER: US 60/404,567
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEC ID NOS: 3
                                                                                                               Sequence 1, Application US/10109498 Publication No. US20030044908A1
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CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: Danish Application
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55; Conservative
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Pred. No. 1.4e-53;
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US-10-255-032-1
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PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                     SEQ ID NO :
                                                                                                      PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR FILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                   APPLICANT: No. US20030100075A10 No. US20030100075A1disk A/S TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
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ORGANISM: Homo sapiens
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/255,032
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                   FILE REFERENCE: 6357-WO
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                                                                                         SOFTWARE: PatentIn version 3.1
ORGANISM: human coagulation Factor VII FEATURE:
                                      TYPE: PRT
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; NAME/KEY: MISC_FEATURE; LOCATION: (1)...(406); LOCATION: (1)...(406); OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate) US-10-255-032-1
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                                                                                                      ; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.2%; Score 726; DB 14; Length 40
Best Local Similarity 36.6%; Pred. No. 1.4e-53;
Matches 155; Conservative 75; Mismatches 157; Indels
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Publication No. US20030130191A1
                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 406
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        Query Match
Best Local Si
Matches 155;
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-10-28
                                                                                                                                                                                      ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                                              TYPE: PRT
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31.2%; Score 726; DB 14; Length 406; 36.6%; Pred. No. 1.4e-53; ative 75; Mismatches 157; Indels 34
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US-10-386-898-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stennicke, Henning Ralf
TITLE OF INVENTION: DIMERIC TF ANTAGONIST
FILE REFERENCE: 6445-200-US
CURRENT APPLICATION NUMBER: US/10/386,898
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: UB. 60/365,935
PRIOR APPLICATION NUMBER: US 60/365,935
PRIOR APPLICATION NUMBER: US 60/365,935
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APPLICANT: No. US20030229018A10 No. US20030229018A1disk Pharmaceuticals, Inc. APPLICANT: Kjalke, Marianne
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                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
                                                                                                                                                        Matches 155; Conservative
                                                                                                                                                                          Query Match 31.2%;
Best Local Similarity 36.6%;
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                                                                                                                                                                                                                                                                                                                  ORGANISM: human coagulation Factor VII FEATURE:
                                                                                                                                                                                                                                                         LOCATION: (1). (406)
OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
                                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE LOCATION: (1)..(406)
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SPCONGGSCKDOLOSYICFCLPAFEGRNCETHKDDOLICVNENGGCEQYCSDHTGTKRSC 112
                                     SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                               ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQC----
                                                                                                                                                     ; Score 726; DB 15;
; Pred. No. 1.4e-53;
75; Mismatches 157
                                                                                                                                                                                                 DB 15;
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                                                                                                                                                            157;
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                                                                                                                                                            Indels 36;
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                                                                                                                                                            Gaps
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US-10-411-037-10
                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-10-411-037-10
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Publication No.
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                                                                                                    Matches
                                                                                                                       Query Match 31.2%; Score 725.5; DB 12; Best Local Similarity 35.4%; Pred. No. 1.9e-53;
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CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
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PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
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PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
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PRIOR FILING DATE: 2002-06-07
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 75
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                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                    151;
52 LEEFVQGNLERECMEEKCSFEEPREVFENTEKTTEFWKQYVDGDQCESNP--
                                              5 LEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC 64
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Chen, Xi
Bowe, Caryn
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No. US20040043446A1
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                                                         Query Match
Best Local Similarity
Matches 151; Conserva
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APPLICANT:
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/387,292 PRIOR FILING DATE: 2002-06-07 PRIOR APPLICATION NUMBER: US 60/391,777
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PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
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PRIOR APPLICATION NUMBER: US 60/396,594
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5 LEBLRHSSLERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC 64
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Hakes, David
Chen, Xi
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                                                                Conservative
                                                           31.2%; Score 725.5; DB 12; Length 462; 35.4%; Pred. No. 1.9e-53; 1tive 69; Mismatches 157; Indels 49;
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    Query Match 31.2%; Score 725.5; DB 16; Best Local Similarity 35.4%; Pred. No. 1.9e-53; Matches 151; Conservative 69; Mismatches 157;
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                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2 SEQ ID NO 10
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PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
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CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
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APPLICANT: Bowe, Caryn
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PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
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PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
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Hakes, David
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Length 462;
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Sequence 10, Application US/10411049
Publication No. US20040082026A1
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CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/328,523 PRIOR FILING DATE: 2001-10-10 PRIOR APPLICATION NUMBER: US 60/344,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON TITLE OF INVENTION: ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Neose Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-10-19
APPLICATION NUMBER: US 60/387,292
FILING DATE: 2002-06-07
                                                                                                                                                                                                                                                                        FILING DATE: 2002-06-25
APPLICATION NUMBER: US 60/396,594
FILING DATE: 2002-07-17
                                                                                                                                                                                                 APPLICATION NUMBER: US 60/407,527
                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/404,249 FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/391,777
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                                                                                                                 version 3.2
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                                                                                                                                                                                                                                                                                                            ; LENGTH: 376
; TYPE: PRT
; ORGANISM: Tropidechis carinatus
US-10-406-031-31
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Publication No. US20040043017A1
                                                                                                                                                                                                 Query Match 31.2%; Score 724; DB 12; Best Local Similarity 35.7%; Pred. No. 1.9e-53; Matches 148; Conservative 73; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: AU 2003901033
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: AU PS1483
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OP INVENTION: FROTHROMBIN ACTIVATING FILE REFERENCE: 15685-002001
CURRENT APPLICATION NUMBER: US/10/406,031
CURRENT FILING DATE: 2003-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Masci, Paul APPLICANT: De Jersey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 NGGSCKDDINSYECWCPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG 160
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  55
                                            61 SLCCGHGTCIDGIGSESCDCRSGWEGRECOREVSELNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                   1 SNSLFBEIRPGNIERECIEEKCSKEEAREVPEDNEKTETFWNVYVDGDQCSSNP-----
                                                                                                                                    1 ANSFLEBLRHSSLERBCIEEICDFEEAKEIFQNVDDTLAFWSKHYDGDQCLVLFLEHPCA 60
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--CHYRGICKDGIGSYTCTCLPNYEGKNCEK-VLYQSCRVDNGNCWHFCKRVQSETQCSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lavin, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          John
                                                                                                                                                                                                              Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ALVLQYLRVPLVDRATCLRSTKF 389
                                                                                                                                                                                                                                                             Length 376;
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US-10-411-049-10

GENERAL INFORMATION:

APPLICANT:

Zopf, David Bayer, Robert DeFrees, Shawn

Hakes, David

APPLICANT: APPLICANT:

Chen, Xi Bowe, Caryn

APPLICANT:

APPLICANT:

; TYPE: PRT; ORGANISM: Homo sapiens US-10-411-049-10

LENGIH: 462

NUMBER OF SEQ ID NOS: 75 SOFTWARE: PatentIn versi SEQ ID NO 10

FILING DATE: 2002-08-28

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RESULT 65 US-10-382-248-36

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; ORGANISM: Homo sapiens US-10-382-248-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/382,248
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/361,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 60/401,661
PRIOR FILING DATE: 2002-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-568C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alsobrook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 82
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 NQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 DKIYVHTKFVPPNYYYVHQNFDRVAYDYDIAIIRMKTPIQFSENVVPACLPTADFA-NEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AESYRLGVDGHSCVAEGDFSCGRNIKARNK-
              298 TGWGYHSSREKEAKRNRTFVLNFIKIFVVPHNECSEVM-----SNMVSENMLCAGILGDR 352
                                                                    236 RRVAQVIIPSTYVPGTTNHDIALLRLHQEVVLTDHVVPLCLPERTFSERTLAFV-RFSLV 294
                                                                                                                 238 LDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQETLV 297
                                                                                                                                                                                                                                181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWELD 237
                                                                                                                                                                                                                                                                                                                                            121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                  113 SPCQNGGSCKDQLQSYICFCLPAFEGRNCE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVFVH-----PNY-----SKSTTDNDIALLHLAQPATLSQTTVPTCLPDSGLAEREL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPWQAVLINEKGEVFCGGTILSPIHVLTAAHCINQTKSV-----KETRRL-----LSV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTLPQDACQGDSGGPHITAYRDTHFITGIISWGEGCARKGKYGVYTKVSKFIPWI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERIKLFWISYSDGDQC------AS 112
                                                                                                                                                                             CPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.9%; Score 671.5; DB 12; Length 419; 34.4%; Pred. No. 6.8e-49; tive 72; Mismatches 125; Indels 79;
                                                                                                                                                                                                                                                                                         -TLEYPCGK-IPILEKRNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                            ---SKPQGRIVGGKVCPKGE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -IVNGMDCKLGE 152
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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RESULT 67
US-09-848-107-1
US-09-848-107-1
; Sequence 1, Application US/09848107
; publication No. US20030170863A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
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Publication No. US20030104978A1
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Native Human Coagulation Factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 426
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 P 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 LKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHDSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 TIVPICLEDSGLAERELNQAGQETLVTGWGYHSSREKEAKKNRTFVLNFIKIPVVPHNEC 331
                                                                                                                                                                                                                        391
                                                                                                                                                                                                                                                                        387 LHNYGVYTKVSRYLDWIHGHIRDKEAP 413
                                                                                                                                                                                                                                                                                                                           331 LQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCAT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 TKLFWISYSDGDQC-----ASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 TLAFWSKHVDGDQCLVLFLEHPCASLCCGHGTCIDGIGSESCDCRSGWEGRFCQ-REVSF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 LNCSLDNGGCTHYCLEEVGWRR-CSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSH 154
                                                                                                                                                                                                                                                                                                                                                                              SEVM----SNMVSENMLCAGILGDRODACEGDSGGPMVASEHGTWELVGLVSWGEGCGL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                    HVVPLCLPERTPSERTLAFV-RFSLVSGWGQLLDRGATA----LELMVLNVPRLMTQDC 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESK---KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQ 271
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                                                                                                                                                                                                                     VGHFGVYTRVSQYIEWLQKLMRSEPRP 417
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Pred. No. 5 5e-48;
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SEQ ID NO 36 LENGTH: 419

TYPE: PRT

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US-10-295-682-1
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 140;
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Best Local
                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10295682 Publication No. US20030100740A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60/236,892
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CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PA 2000 00734
PRIOR FILING DATE: 2000-05-03
                     SEQ ID NO 1
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                                      PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
                                                                                                                                                                                                                                                                                                      APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
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LENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 28.4%; Score 661; DB 10;
Similarity 36.2%; Pred. No. 5.5e-48;
40; Conservative 71; Mismatches 140;
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                                                                                          331 LQQSRXVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCAT 390
                                                                                                                                       332 SEVM-----SNMVSENMICAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGL 386
391 VGHFGVYTRVSQYIEWLQKLMRSEPRP 417
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                                                                                                                                                                                             HVVPLCLPERTFSERTLAFV-RFSLVSGWGQLLDRGATA-----LELMVLNVPRLMTQDC
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                                            LHNYGVYTKVSRYLDWIHGHIRDKEAP 413
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US-10-038-854-6
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Publication No. US20040022781A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
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                                                                                  Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
Smithson, Glennda
Millet, Isabelle
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Malyankar, Uriel M
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Rastelli, Luca
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Gangolli, Esha A
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Kekuda, Ramesh
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                                                                                                                                                                                RESULT 70
US-10-406-031-30
                GENERAL INFORMATION:
APPLICANT: Masci, Paul Fantaleone
APPLICANT: De Jersey, John
APPLICANT: Lavin, Martin
TITLE OF INVENTION: PROTHROMBIN ACTIVATING PROTEIN
FILE REFERENCE: 15685-002001
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Best Local Similarity
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                                                                                                                                       Sequence 30, Application US/10406031 Publication No. US20040043017A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PAIM NUMBER OF SEQ ID NOS: 411
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CURRENT APPLICATION NUMBER: US/10/406,031
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/284,447
FILING DATE: 2001-04-18
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APPLICATION NUMBER: 60/269,814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 LEEFVQGNLERECLEEKCSFEEAREVFENTERTTEFWKQYVDGDQCESNP-----CL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVAGEHNIEETEHTEQKRN 228
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                                                                                                                                                                                                                                                              CQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRYVNWI 387
                                                                                                                                                                                                                                                                                                     CEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                   TGWG--YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDA 355
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32.6%;
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Pred. No. 1.4e-45;
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US-10-406-031-30
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US-10-406-031-28
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PRIOR FILING DATE: 2003-03-07
PRIOR PRILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 158;
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Best Local :
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Masci, Paul Pantaleone
APPLICANT: De Jersey, John
APPLICANT: Lavin, Martin
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: AU PS1483
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
OTHER INFORMATION: Xaa = any amino acid
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CURRENT FILING DATE: 2003-04-02
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FEATURE:

FEATURE:

NAME/KEY: VARIANT

LOCATION: 45, 48, 70, 124, 126, 197, 210, 227, 258, 261, 312, 314, LOCATION: 347, 365, 378, 419, 423, 437, 441, 451
                                                                                                         LOCATION: 41, 50, OTHER INFORMATION:
                                                                                                                                                                NAME/KEY: VARIANT
                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 NQAGQETLYTGWGYHSSREKEAKRNRTFVLNFIK-IPVVPHNECSEVMSNMVSENMLCAG 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LCCGHGTCIDGIGSFSCDCRSGWEGRFCOREVSFLNCSLDNGGCTHYCLEEVGWRRCSCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 NSLFEEFR-GNIERECIEE-CSKEEAREVFED-EKTETFWNVYVDGDQCSSNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKQ-DFGI VSGFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKWELDLDIKEVFVH---PNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAEREL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGMDCKLGECPWQAVL---DEKVFCGGTILSPIYVLTAAHCINQT-KISVVVGBIDISRK 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -CHYRGICKDGIGSYICICL--YEGKNC--EVLYKSCRVDNGNCWHFC--KVQNDQCSCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -YDTLPDACQGDSGGPHITAYRDTHFITG-ISWGEGCA-KGKYGVYTKVSKFIPWI 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETL---LSVDKIYVHKFVPPYF-DVYDYDIAIIOMKTPIQFSENVVPACLPTADFANQVL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                            79, 114, 154, 177, : Xaa = small amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RIGPSNTLKVVPYVDRHTC--MLSSFITP-MFCAG
                                                                                                               255, 272, 290
acid residue
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LOCATION: 296, 300, OTHER INFORMATION: OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: Xaa = acidic amino acid residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 72, 229-230, 256
OTHER INFORMATION: Xaa = charged amino acid residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetically generated peptide
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NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 193.
OTHER INFORMATION:
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les 138; Conserv
                                                               281 SGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVS 340
                                                                                                                                                         234 WELDLDIKEVFVHPNY---
                                                                                                                                                                                                        213 MDCKLGECPWQAXLXXXXXXXFCGGTTLSPIXVLTAAHCIXXXXXXXSVXVGEIXXSRXXX 272
                                                                                                                                                                                                                                                                                                                                              122 PGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTED-----QEDQVDP--RLIDG 173
                                                                                                                                                                                                                                                                                                                                                                                             95 -CHYXGXCKDGIGSYTCTCLXXYEGKNCEXXLX-XSCRXXNGNCWHFCKXVQXXXQCSCA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 NSLXEEXXXGNIERECIEEXCSKEEAREXEXDXEKTEXFWNVTVDGDQCSSNP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCA 121
                   ADFAXXVLMKQ-DXGIXSGFGXXX-----XXXXXSXXLXXXXVPYVDRHTCMXSSXXXII 385
                                                                                                                                                                                                                                                 KMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEK 233
                                                                                                                                                                                                                                                                                                  EXYXLGXDGHSCVAXGXFSCGRNIKXRNKREASLPDFVQSXXXXXKKSDNPSPDIRIXNG 212
                                                                                                           Conservative
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hydrophobic amino acid residues
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acidic amino acid residues
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Xaa = independently absent
any amino acid residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.3%; Score 611.5; DB 12; Length 456; 32.6%; Pred. No. 1e-43; tive 52; Mismatches 196; Indels 37;
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                                                                                                                                                         -SKSTTDNDIALLHLAQPATLSQTIVPICLPD 280
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US-10-020-141-8
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PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 21
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10020141
Publication No. US20030092013A1
GENERAL INFORMATION:
APPLICANT: MCCarthy, Jeanette
APPLICANT: Ableson, Allen
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.2%;
Best Local Similarity 29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/313,097
PRIOR FILING DATE: 2001-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/020,141
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: MMI-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 XWI 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103
                                                                                                                                                                                                                                394 SLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRY 453
                                                                                                                                                                                                                                                                            199 VLIHPSWYLTAAHCM-----DES----KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPNY 249
                                                                                                                                                                                                                                                                                                                           336 CGLRP--LFEKKSLEDKTERELLESYIDGRIVEGSDAEIGMSPWQVMLFRKSPQELLCGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 QYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW----CY 275
                                           513 ANVGKGOPSVLOVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGPF
                                                                                                                                           454
                                                                                                                                                                                  250 S-KSTTDNDIALIHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWG-YHSSRE
                                                                                                                                                                                                                                                                                                                                                                         141 CG-REWKRMEKKRSHLKRDTEDQEDQVDFRLIDGKWTRRGDSFWQVVLL-DSKKKLACGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                        276 VAGKPGDFGYCDLNYCEEAVBEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEAD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 PGYKLGD----DLLQCHPAV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 PDSSTTGPWCYTTDPTVRRQECSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRGQ 219
365 V--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 --SGWEGRFC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATDVFWAKYTACETART-PRDKLAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CLEGNCAEGLGTNYRGHVNITRSGIECQLWRSRYPHXPEINSTTHPGADLQENFCRN 159
                                                                                       KEAKRNRTFYLNFIKIPYYPHNECSEVMSNMYSENMLCAGIL---GDRQDACEGDSGGPM 364
                                                                                                                                           NWRENLDRDIALMKIKKPVAFSDYIHPVCLPDRETA-ASILQAGYKGRVTGWGNIKETWT 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Mismatches 161; Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 562.5; DB 14; Length 622; Pred. No. 2.3e-39;
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US-10-406-031-28

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US-10-214-932-116
; Sequence 116, Application US/10214932
; Publication No. US20030100707A1
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Publication No. US20030099957A1
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CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/325,930
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 4
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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-006
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GENERAL INFORMATION:

APPLICANT: GRIFFIN, JOHN H.

APPLICANT: GRIZOFF, ELIZABET
APPLICANT: GRIZOFF, ELIZABET
APPLICANT: PELLEQUER, JEAN-L

APPLICANT: GETZOFF, ELIZABETH D.
APPLICANT: PELLEQUEX, JEAN-IUC
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS
FILE REFERENCE: 4198-4001US1
CURRENT APPLICATION NUMBER: US/10/172,712

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RESULT 75
US-10-172-712-29
; Sequence 29, Application US/10172712
; Publication No. US20030125232A1
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Best Local Similarity 29.1%; Pred. No. 2.3e-39;
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APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
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ORGANISM: Homo sapiens
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US-10-072-012-410
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PRIOR APPLICATION NUMBER: 60/298,578
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
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                                                                                                                                                                                                                                                              Sequence 410, Application US/10072012
Publication No. US20040033493A1
                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATDVFWAKYTACETART-PRDKLAA 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGPF 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGPM 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLIHPSWVLTAAHCM----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPNY
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                 Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach,
                                                                                                 Gangolli, Esha
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Shimkets, Richard
                                                                       Padigaru,
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Valerie
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SEQ ID NO 410
LENGTH: 799
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PRIOR FILING DAYE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DAYE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DAYE: 2001-02-02
PRIOR FILING DAYE: 2001-02-02
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PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
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CURRENT FILING DATE: 2002-01-31
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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PRIOR FILING DATE: 2001-02-07
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TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 22.0%; Score 510.5; DB 12; Local Similarity 34.9%; Pred. No. 8.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/267,459
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                                                                                                                                                                                     593 ALIADRWVITAAHCFQEDSMASPKLWTVFLGK--MRQNSRWPGEVSFKVSRLFLHPYHEE 650
                                                                                                                                                                                                                                 199 VLIHPSWYLTAAHCMDE----SKKL-LVRLGEYDLRRWEKW--ELDLDIKEVFVHPNYSK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                      97 NCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 FWSKHVDGDQCLVLPLEHPCASLCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFL 96
SN---TLQKVDVQLVPQDLCSEAYRYQVSPRMLCAGYRKGKKDACQGDSGGPLVCREPSG
                                            RINTIFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SPHG
                                                                                          DSHDYDVALLQLDHPVVYSATVRPVCLP----ARSHFFEPGQHCWITGWG--AQREGGPV 704
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
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Pena, Carol E. A
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SEQ ID NO 416
LENGTH: 799
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                                                                    Query Match 22.0%; Score 510.5; DB 12; Best Local Similarity 34.9%; Pred. No. 8.7e-35; Matches 137; Conservative 52; Mismatches 141;
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APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine B.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
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PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-02-02
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PRIOR APPLICATION NUMBER: 60/265,395
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                                                                                                                                                                                                  LENGTH: 79
TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/267,459
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                                                                                                                                                                                 ORGANISM: Mus musculus
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762 RWFLAGIVSWGLGCGRPNFFGVYTRVTRVINWI 794
436 YYSLYNQSDPC-----PGEFLCSVNGLCVPACDGIK----DCPNGLDERNCVCRAMF- 483
                                    40 FWSKHVDGDQCLVLPLEHPCASICCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFL 96
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Taupier Jr, Raymond J. Gusev, Vladimir Y. Colman, Steven D. Wolenc, Adam R.
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Anderson, David W.
Rastelli, Luca
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Grosse, William M.
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b. US20040033493A1
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                                                                               Indels
                                                                                                                       Length 799;
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US-09-981-151A-87
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Sequence 87, Application US/09981151A Publication No. US20030212256A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR FILING DATE: 2000-10-17
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/242,482
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION UNUMBER: 60/241,243
PRIOR FILING DATE: 2000-10-17
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PRIOR FILING DATE: 2000-10-17
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                PRIOR APPLICATION NUMBER: 60/242,612
PRIOR FILING DATE: 2000-10-23
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                                                       APPLICATION NUMBER: 60/242,611 FILING DATE: 2000-10-23
APPLICATION NUMBER:
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MacDougall, John R
Malyankar, Muriel M
Smithson, Glennda
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Burgess, Catherine E
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Padigaru, Muralidhara
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Stone, David J
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    60/242,880
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; OTHER INFORMATION: Description of Artificial Sequence: Trypsin-like ; OTHER INFORMATION: Berine protease Consensus Sequence US-09-981-151A-87
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR APPLICATION NUMBER: 60/241,050
PRIOR APPLICATION NUMBER: 60/241,050
PRIOR RILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,063
PRIOR APPLICATION NUMBER: 60/241,063
PRIOR FILING DATE: 2000-10-17
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PRIOR APPLICATION NUMBER: 60/242,881
PRIOR FILING DATE: 2000-10-24
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APPLICANT: Gerlach, Valerie
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/981,151A CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                             APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-168
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Stone, David J
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Malyankar, Muriel M
Smithson, Glennda
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Gangolli, Esha A
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Taupier Jr, Raymond
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SEQ ID NO 96
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: 60/242,881
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PRIOR APPLICATION NUMBER: 60/242,612
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PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/242,880
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Local Similarity 45.0%; Pred. No. 1.4e-33;
nes 108; Conservative 32; Mismatches 85; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                              169 RLIDGKWITRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDES--KKLLVRLGEY 226
172 CAGGLEGGKDACQGDSGGPLVCN-DPRWVLVGIVSWGSYGCARPNKPGVYTRVSSYLDWI 230
                                                                                                         119 ---PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNWL
                                                                                                                                                            287 ELNQAGQETLYTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN--MVSENML 344
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                                       CAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGE-GCGLLHNYGVYTKVSRYLDWI 403
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US-10-042-865-155
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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   APPLICANT:
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Boldog, Ference L
Grosse, William M
Alsobrook II, John I
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
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Spytek, Kimberly
                                                                                          Guo,
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Miller, Charles E
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Burgess, Catherine E
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US-10-072-012-804
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 155
LENGTH: 230
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CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
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PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
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APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DLSSGEETQ-TVKVSKVIVHENYNPSTYDNDIALLKLSEPVTLSDTVRPICLPSSGYNV- 118
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                                                                  Ratelli, buca
Ratler, Charles E.
Miller, Charles E.
Parlach, Valerie
                   Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNML 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN--MVSENML 344
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Malyankar, Uriel M
Millet, Isabelle
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Gunther, Erik
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                                                                                                                                          Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
                                                                                                                                                                                                                                                    Zerhusen, Bryan
Patturajan, Mee
Wolenc,
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  Adam R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.0%; Score 488.5; DB 12; Length 230; 45.0%; Pred. No. 1.4e-33;
                                                                                                                                                                                                                                                       Meera
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RESULT 82 US-10-072-012-812

; Sequence 812, Application US/10072012; Publication No. US20040033493A1; GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar APPLICANT: Spytek, Kimberly APPLICANT: Zerhusen, Bryan APPLICANT: Patturajan, Meera

Patturajan, Meera

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APPLICANT:
APPLICANT:
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LENGTH: 230
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Best Local S
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-258
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION UNMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
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CURRENT FILING DATE: 2002-01-31
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PRIOR FILING DATE: 2001-02-02
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PRIOR FILING DATE: 2001-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Trypsin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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                                       345 CAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGE-GCGLLHNYGVYTKVSRYLDWI 403
                                                                                    119 ---PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNWL 171
                                                                                                                              287 ELNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPYVPHNECSEVMSN--MVSENML 344
172
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                                                                                                                                                                          DLSSGBETQ-TVKVSKVIVHÞNYNPSTYDNDIALLKLSEÞVTLSDTVRÞICLÞSSGYNV- 118
CAGGLEGGKDACQGDSGGPLVCN-DPRWVLVGIVSWGSYGCARPNKPGVYTRVSSYLDWI
                                                                                                                                                                                                                    DLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAER 286
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
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45.0%; Pred. No. 1.4e-33;
tive 32; Mismatches 85
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172 CAGGLEGGKDACQGDSGGPLVCN-DPRWYLVGIVSWGSYGCARENKPGVYTRVSSYLDWI 230

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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 812
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION UNMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
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CURRENT FILING DATE: 2002-01-31
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PRIOR FILING DATE: 2001-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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APPLICATION NUMBER: 60/266,975
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345 CAGIIGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGE-GCGLLHNYGVYTKVSRYLDWI 403
                                                             119 ---PAGTICTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNWL 171
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                                                                                                                                                                                DLRRWEKWELDLDIKEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAER 286
                                                                                                       ELNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPVYPHNECSEVMSN--MVSENML 344
                                                                                                                                                 DLSSGEETQ-TVKVSKVIVHPNYNPSTYDNDIALLKLSEPVTLSDTVRPICLPSSGYNV- 118
                                                                                                                                                                                                                                 RIVGGSEANIGSFFWQVSLQYRGGRHFCGGSLISPRWVLTAAHCVYGSAPSSIRVRLGSH 60
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Rieger, Daniel K.
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Grosse, William M.
Alsobrook II, John P.
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Pena, Carol E. A
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Miller, Charles E.
Gerlach, Valerie
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45.0%;
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matches 85; Indels 15;
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                                                        Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                   SEQ ID NO 135
LENGTH: 230
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION UNMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
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PRIOR FILING DATE: 2001-01-05
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CURRENT FILING DATE: 2002-09-20
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                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 227 SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/318,700 PRIOR FILING DATE: 2001-09-12
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                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Trypsin-like OTHER INFORMATION: Berine protease Consensus Sequence
                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   TYPE: PRT
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169 RLIDGKMTRRGDSPMQVVLLDSKKKLACGAVLIHPSWVLTNAHCMDES--KKLLVRLGEY 226
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Grosse, William M
Lepley, Denise M
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Tchernev, Velizar T
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Miller, Charles E
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Stone, David J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Padigaru, Muralidhara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boldog,
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                                                          Conservative
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                                                                              21.0%;
45.0%;
                                                          %; Score 488.5; DB 12;
%; Pred. No. 1.4e-33;
32; Mismatches 85;
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US-10-032-139-66
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                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-228
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                                                           PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,940 PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/282,981 PRIOR FILING DATE: 2001-04-11
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                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/283,656
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FILING DATE: 2001-08-17
                   APPLICATION NUMBER: 60/313,331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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Gunther, Erik
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Grosse, William M
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Grosse, William M
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Fernandes, Elma R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorman, Linda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lepley, Denise M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spytek, Kimberly A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edward S
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US-10-074-978A-221
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SDFTMARE: Patentin Ver. 2.1
SEQ ID NO 66
LENGTH: 230
TYPE: PRT
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Best Local Similarity
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                                             APPLICANT: Gunther, Erik
APPLICANT: Stone, Dave
APPLICANT: Stone, John
APPLICANT: Peyman, John
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
TITLE DF INVENTION, HOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-269
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CURRENT APPLICATION NUMBER: US/10/074,978A CURRENT FILING DATE: 2003-01-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 CAGGLEGGKDACQGDSGGFLVCN-DPRWVLVGIVSWGSYGCARPNKPGVYTRVSSYLDWI
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Moore, No. US20040010119Allle
Shenoy, Suresh
Edinger, Shlomit
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Vernet, Corine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casman, Stacie
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Rastelli, Luca
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Malyankar, Uriel M
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Heyes, Melvin P
                                                                                                                                                                                                                                                                                                                                                                                                                  Mezes, Peter S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patturajan, Meera
                                                                                                                                                                                                                                                                                                                       Pena, Carol E A
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45.0%;
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US-10-074-978A-222
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LENGTH: 230
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Best Local :
                                                                                                                                                                                                                                                                             GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                             Sequence 222, Application US/10074978A Publication No. US20040010119A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 547
SOFTWARE: PatentIn Ver. 2.1
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PRIOR APPLICATION NUMBER: 60/268,646
PRIOR FILING DATE: 2001-02-14
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                                                         APPLICANT:
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     APPLICANT:
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                                                                                              APPLICANT:
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                                      PPLICANT
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APPLICATION NUMBER: 60/280,899
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APPLICATION NUMBER: 60/330,293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/268,221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atch 21.0%; Score 488.5; DB 15; Length 230; cal Similarity 45.0%; Pred. No. 1.4e-33; 108; Conservative 32; Mismatches 85; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                         172 CAGGLEGGKDACQGDSGGPLVCN-DPRWVLVGIVSWGSYGCARPNKPGVYTRVSSYLDWI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                             345 CAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGE-GCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 DLRRWEKWELDLDIKEVFYHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLFDSGLAER 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLSSGEETQ-TVKVSKVIVHENYNPSTYDNDIALLKLSEEVTLSDTVREICLESSGYNV- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNML 171
Tchernev, Velizar 'Malyankar, Uriel M
                                  Ballinger, Robe
Vernet, Corine
                                                                                                                                                                                                                    Spytek, Kimberly A
Guo, Xiaojia (Sasha
                                                                       Patturajan, Meera
Blalock, Angela
                                                                                                           Casman, Stacie
Boldog, Ferenc
                                                                                                                             Liu, Xiahong
Casman, Stacie
                                                                                                                                                                   Kekuda, Ramesh
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                                                       Robert
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         US-10-055-569A-96
                          RESULT 87
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US-10-074-978A-222
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PRIOR APPLICATION NUMBER: 60/335,109
PRIOR FILING DATE: 2001-031
PRIOR APPLICATION NUMBER: 60/312,284
PRIOR APPLICATION NUMBER: 60/216,284
PRIOR APPLICATION NUMBER: 60/266,496
PRIOR APPLICATION NUMBER: 60/276,703
PRIOR APPLICATION NUMBER: 60/276,703
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/330,293
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/322,127
PRIOR FILING DATE: 2001-11-21
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APPLICANT: Millet, Habelle
APPLICANT: Myllet, John
APPLICANT: Beyman, John
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/310,797
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/268,646
PRIOR FILING DATE: 2001-02-14
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PRIOR FILING DATE: 2001-04-02
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                           227 DLRRWEKWELDLDIKEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLEDSGLAER 286
                                                                                                                                                                                                                                                                                                                                                                   169 RLIDGKMTRRGDSFWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDES--KKLLVRLGEY 226
                                                 345 CAGIIGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGB-GCGLLHNYGVYTKVSRYLDWI 403
                                                                                                        119 ---PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNWL 171
                                                                                                                                                               287 ELNQAGQETLVTGWGYHSSREKEAKKNRTFVLNFIKIPVVPHNECSEVMSN--MVSENML 344
                                                                                                                                                                                                                   61 DISSGEETQ-TVKVSKVIVHPNYNPSTYDNDIALLKISEPVTISDTVRPICIPSSGYNV- 118
                                                                                                                                                                                                                                                                                                                              1 RIVGGSEANIGSFPWQVSLQYRGGRHFCGGSLISPRWVLTAAHCVYGSAPSSIRVRLGSH 60
ĊĀĠĠĹEĠĠKĎĀĊQĠĎŚĠĠĎĹŸĊN-DPRWVĹŸĠĹŸŚWĠŚYĠĊĀRPNKPĠŸŶŤŔŶŚŚŶĹĎŴĨ 230
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Edinger, Shlomit
Gunther, Erik
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Rastelli, Luca
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Moore, No. US20040010119Allle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pena, Carol E A
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                                                                                                                                                                                                                                                                                                                                                                                                                                         21.0%; Score 488.5; DB 15; Length 230;
45.0%; Pred. No. 1.4e-33;
htive 32; Mismatches 85; Indels 15;
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SOFTWARE Patentin Ver. 2.1
SEQ ID NO 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.0%; Score 488.5; DB 16; Best Local Similarity 45.0%; Pred. No. 1.4e-33; Matches 108; Conservative 32; Mismatches 85;
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr., Raymond J
APPLICANT: Anderson, David W
TITLE OF INVENTION: No. US20040024181Alel Human Proteins, Polynucleotides Encoding
TITLE OF INVENTION: Methods of Using the Same
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PRIOR APPLICATION NUMBER: 60/245,315
PRIOR FILING DATE: 2000-11-02
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PRIOR APPLICATION NUMBER: 60/244,995
PRIOR FILING DATE: 2000-11-01
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PRIOR FILING DATE: 2000-10-26
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TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/243,863
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RIOR APPLICATION NUMBER: 60/245,029
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                                                                             287 ELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN--MVSENML 344
                                                                                                                                                                                                                                            227 DLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAER 286
                                                                                                                                                                                                                                                                                                                                                                                                                                  169 RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDES--KKLLVRLGEY 226
119 ---PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNWL 171
                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                           1 RIVGGSEANIGSFFWQVSLQYRGGRHFCGGSLISFRWVLTAAHCVYGSAPSSIRVRLGSH 60
                                                                                                                                                          Spytek, Kimberly A
Gilbert, Jennifer
Casman, Stacie
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Gunther, Erik
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Edinger, Shlomit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shenoy, Suresh
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RESULT 88
US-10-051-874-101
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CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/325,306
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 60/330,336

PRIOR FILING DATE: 2001-10-18

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/261,376

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/272,409
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/276,777
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                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/291,672
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
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Casman, Stacie J
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Malyankar, Uriel M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10051874 o. US20040005557A1
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Stone, David J
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Grosse, William M
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Taupier Jr, Raymond J
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Mezes, Peter D
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Millet, Isabelle
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                                                                                                                                                                                                 2001-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catherine B PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 72
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APPLICANT:
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                                                                                                                                                       Matches
                                                                                                                                                                                                Query Match
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APPLICANT: Spytek, Kimberly A
APPLICANT: Rastelli, Luca
APPLICANT: Herrman, John L
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-750
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CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/194,314
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/225,693
PRIOR FILING DATE: 2000-08-16
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Tryp_SPc. OTHER INFORMATION: Trypsin-like serine protease domain sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:Consensus OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 LNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPYVPHNECSEVMSN--MYSENMLC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 LRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERE 287
227 DLRRWEKNELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATISQTIVPICLPDSGLAER 286
                                                                                                              169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LSSGEETQ-TVKVSKVIVHPNYNPSTYDNDIALLKLSBPVTLSDTVRPICLPSSGYNV-- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVGGSEANIGSFEWQVSLQYRGGRHFCGGSLISPRWYLTAAHCVYGSAPSSIRVRLGSHD
                                                                1 RIVGGSEANIGSFPWQVSLQYRGGGRHFCGGSLISPRWVLTAAHCVYGSDSSIRVRLGSH 60
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Similarity 44.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGE-GCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PAGTTCTVSGWG----RTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNMLC 171
                                                                                                              RLIDGKMTRRGDSPWQVVL-LDSKKKLACGAVLIHPSWVLTAAHCM-DESKKLLVRLGEY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandes, Elma R
Taupier, Raymond J
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                                                                                                                                                     32;
                                                                                                                                                     Score 482; DB 12;
Pred. No. 5.1e-33;
32; Mismatches 86;
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98
                                                                                                                                                         Indels 14;
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PRIOR APPLICATION NUMBER: 60/179,982
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR APPLICATION NUMBER: 09/657,968
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
NUMBER: OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 658
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Publication No. US20030119168A1
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: TRANSMEMERANE SERINE PROTEASES,
TITLE OF INVENTION: METHODS BASED THEREON
FILE REFERENCE: 24745-1607
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CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/213,124
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/234,840
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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les 125; Conserv
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579 LCSEVYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 638
                                          330 BCSEVMSNMVSENMLCAGIIGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
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                                                                                                                                          SQTIVPICLPDSGLAERELNOAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                               SAAVRPVCLP----ARSHFFBPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 578
                                                                                                                                                                                         DEEHCECGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 467
                                                                                                                                                                                                                                                                                                                                        DQE-----DQVDPRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
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33.3%; Pred. No. 9e-32;
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LENGTH: 658
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CURRENT FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 611
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Daniel Vanna Siev
TITLE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic Us
TITLE OF INVENTION: Thereof
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APPLICANT: Edwin L. Madison
APPLICANT: Edwin L. Ong
APPLICANT: Edwar O. Ong
APPLICANT: Jiunn-Chern Yeh
APPLICANT: Corvas International, Inc.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES,
TITLE OF INVENTION: METHODS BASED THEREON
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ORGANISM: Homo Sapien
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George P. Vlasuk
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                           THE ENCODED PROTEINS AND
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GENERAL INFORMATION:
APPLICANT: Edwin L. Madison
APPLICANT: Joseph Edward Sem;
APPLICANT: George P. Vlasuk
APPLICANT: Scott Jeffrey Kem;
APPLICANT: Mallareddy Komandl
APPLICANT: Daniel Vanna Siev
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CURRENT APPLICATION NUMBER: US/09/776,191
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/213,124
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/234,840
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/179,982
PRIOR APPLICATION NUMBER: 60/179,982
PRIOR RILING DATE: 2000-02-03
PRIOR RILING DATE: 2000-02-03
PRIOR RILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-02-18
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CURRENT APPLICATION NUMBER: US/10/156,214A
CURRENT FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 611
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 72
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TYPE: PRT
                                                                                                                                                                 TITLE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic UTITLE OF INVENTION: Thereof
                                                                                                                                     FILE REFERENCE: 24745-1611
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Local Similarity 33.3%; Pred. No. 1.2e-31;
nes 125; Conservative 52; Mismatches 144; Indels
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                                                                                                                                                                                                                   Mallareddy Komandla
Daniel Vanna Siev
                                                                                                                                                                                                                                                                     Joseph Edward Semple
George P. Vlasuk
Scott Jeffrey Kemp
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US-10-156-214A-8
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US-10-600-187-7
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                                                                                                                                   US-10-600-187-7
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Best Local :
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                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 98
SEQ ID NO 7
                                                                Matches
                                                                              Query Match 20.4%; Score 473.5; DB 16; Best Local Similarity 37.9%; Pred. No. 3.1e-32;
                                                                                                                                                                                                                                                                                                              APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/10/600,187
CURRENT FILING DATE: 203-06-20
PRIOR APPLICATION NUMBER: US/09/654,600A
PRIOR APPLICATION NUMBER: US/09/654,600A
PRIOR APPLICATION NUMBER: 09/421,213
                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-10-20
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                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                  OTHER INFORMATION: Factor 7
                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                   LENGTH: 255
                                                                                                                                                                                                                                                                    1998-02-20
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                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
1 RIVGGKVCPKGECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEGVYTRITGVISWI 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAAVR PVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------
                             RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK----KLLVRLGE 225
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                                                                Conservative 52; Mismatches
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US-10-172-712-28
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SEQ ID NO 28
LENGTH: 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 141; Conservative
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ORGANISM: Homo sapiens
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Sequence 28, Application US/10172712
Publication No. US20030125232A1
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APPLICANT: GRIZOFF, ANDREW J.
APPLICANT: GETZOFF, ELEXABETH D.
APPLICANT: PELLEQUER, JEAN-LUC
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS
FILE REFERENCE: 4198-4001US1
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PRIOR APPLICATION NUMBER: 60/298,578
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 KDCGTEKCFDETRYEYLEGGDRWARVRQGHVEQCECFGGRTWCEGTRHTACLSSPCLN-- 252
342 NMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLD 401
                                                                                                                                                                                                                                                                                                                                                                         419 HPWLAAIYIGDS----FCAGSLVHTCWVVSAAHCFSHSPPRDSVSVVLGQHFFNRTTDVT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 LTRVQLSPDLLATLPEPASPGRQACGRRHKKRTFLR------PRIIGGSSSLPGS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 --GGTCHLIVATGTTVCACPPGFAGRLCNIEPD-ERCFLGNGTGYRGVASTSASGLSCLA 309
                                                                                                                                                                                                                                                                                                   236 LDLDIKEVFVHPNYSK-STTDNDIALLHLAQP----ATLSQTIVPICLPDSGLAERELNQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CGHGTC--IDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SPW--QVVILDSKKKLACGAVLIHPSWVLTAAHCMDES---KKLLVRLGEYDLRRWEKWE 235
                                                                                                                                        AGQETLVTGWGY-----HSSREKEAKRNRTFVLNFIKIPVVPHNECS--EVMSNMVSE 341
                                                                                                                                                                                                                         QTFGIEKYIPYTLYSVENPSDHDLVLIRLKKKGDRCATRSQFVQPICLPEPG----STFP 530
                                                                         AGHKCQIAGWGHLDENVSGYSSSLREA------LVPLVADHKCSSPEVYGADISP 579
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US-09-888-615-113
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APPLICANT: CARREPEL, SEAN
APPLICANT: CHARNEZEL, GLEN
APPLICANT: CHARNEZEL, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT PILING DATE: 2001-06-26
PRIOR APPLICATION UNMER: 60/214,047
PRIOR APPLICATION UNMER: 60/214,047
PRIOR FILING DATE: 2001-06-26
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                                                           RESULT 97
US-09-978-95A-169
VS-09-978-95A-169
Sequence 169, Application US/09978295A
; Patent No. US20020156006A1
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SEQ ID NO 113
LENGTH: 802
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                GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PLOWMAN,
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 WIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                          723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 V----CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
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                                                                                                                                                                                                  783 YFGVYTRITGVISWI 797
                                                                                                                                                                                                                                             389 NYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                             672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                                                                                                                                                                                                                                                                                                                                                                        SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKKNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                                                       LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWPLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                                                                                  ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
Baker Kevin P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.2%; Score 470; DB 9; Length 802; ilarity 33.1%; Pred. No. 2.5e-31; Conservative 52; Mismatches 145; Indels
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILLING DATE: 1997-11-21
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PRIOR FILLING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Ef, Ellen
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR TILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/06220
PRIOR PLICATION NUMBER: 60/06220
PRIOR PLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/077450
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC27
PRIOR APPLICATION NUMBER: 60/078004
FRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
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PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Desnoyers, Luc
Eaton, Dan
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E.
Goddard, Audrey
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Kuo, Sophia S.
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PRIOR APPLICATION NUMBER: 60/081836
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PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
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PRIOR APPLICATION NUMBER: 60/080165
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
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PRIOR APPLICATION NUMBER: 60/081195
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PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
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PRIOR APPLICATION NUMBER: 60/081955
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PRIOR APPLICATION NUMBER: 60/078910 PRIOR FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079920 FILING DATE: 1998-03-30 PILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079689 APPLICATION NUMBER: 60/079664 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/078939 DATE: 1998-03-20 1998-03-27 1998-03-27 60/079663

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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/085582
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52; Mismatches 145;
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/062250
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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Grimaldi, J. C
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR APPLICATION NUMBER: 60/083495
PRIOR BELLING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
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PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29 PRIOR PRIOR PRIOR PRIOR DR APPLICATION NUMBER: 60/081952
RR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081838
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DR APPLICATION NUMBER: 60/082568
DR FILING DATE: 1998-04-21
DR FILING DATE: 1998-04-21 OR FILING OATE: 1998-05-05

OR APPLICATION NUMBER: 60/084414

OR APPLICATION NUMBER: 60/084441

OR APPLICATION NUMBER: 60/084441

OR FILING DATE: 1998-05-06

OR APPLICATION NUMBER: 60/084637 OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085339
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OR FILING DATE: 1998-05-13
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084627 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084643 APPLICATION NUMBER: 60/084598 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084639 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084600 PILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 60/084627

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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napole,
APPLICANT: Filvaroff, Elles,
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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PRIOR APPLICATION NUMBER: 60/085579
PRIOR APPLICATION NUMBER: 60/085580
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
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Roy, Marg
Shelton,
Stewart,
                                                                                                                                                                           Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                  Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                        Botstein, David
Desnoyers, Luc
                                                                                Pan,
                                                                                               Napier, Mary A.
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o. US20020192706A1
                                                           Paoni,
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                                                                                                                                                                                                                                                                                                       Wei-Qiang
                                        Margaret Ann
                                                                              James;
                                                           Nicholas F
David L. Timothy
                                                                                                                                                                                                                                                                                                                                             Napoleon
f, Ellen
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR PILING DATE: 1997-11-21
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIDR APPLICATION NUMBER: 60/062250
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DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/079294
DR FILING DATE: 1998-03-25
DR APPLICATION NUMBER: 60/079656
DR FILING DATE: 1998-03-26
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FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-03-20
                  APPLICATION NUMBER: 60/080334 FILING DATE: 1998-04-01
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/081070
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Williams, P. Mickey
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083558
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/082804
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            APPLICATION NUMBER: 60/084639
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/084637
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PRIOR APPLICATION NUMBER: 60/085689
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085339
OR PILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15
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  783
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                                                                                                                                                                                                                             EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR
                                                                                                                                                                                                                                                               ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHENYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                       DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCAS---LCCGHGTCI----DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
YFGVYTRITGVISWI
                                                                        LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                       SQTIVPICLPDSGLAERELNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPVVPHN 329
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Pred. No. 2.5e-31;
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Gaps

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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan US-09-978-189-169 RESULT 101 Sequence 169, Appublication No. APPLICANT:
APPLICANT: Botstein, David Desnoyers, Luc Ferrara, Napoleon Filvaroff, Ellen Application US/09978189 5. US20030004102A1 שי

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CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
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FILING DATE: 1997-11-13
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FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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                                               APPLICATION NUMBER: 60/079786 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
Kljavin, Ivar J.
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PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322 PRIOR FILING DATE: 1956-04-22
PRIOR APPLICATION NUMBER: 60/082796 PRIOR PRIOR FILING DATE: 1998-04-28 PRIOR APPLICATION NUMBER: 60/083392 OR APPLICATION NUMBER: 60/083554
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083558
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OR FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/081952
APPLICATION NUMBER: 60/081952
-\*\*\*This DATE: 1998-04-15 APPLICATION NUMBER: FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071 APPLICATION NUMBER: 60/081070 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 FILING DATE: APPLICATION NUMBER: 60/082700 FILING DATE: APPLICATION NUMBER: 60/082804 FILING DATE: APPLICATION NUMBER: 60/082569 PILING DATE: 1998-04-21 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04 APPLICATION NUMBER: APPLICATION NUMBER: 60/081817 APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 FILING DATE: 1998-04-09 FILING DATE: 1998-04 APPLICATION NUMBER: FILING DATE: 1998-04-08 FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083545 APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 FILING DATE: 1998-04-01 1998-03-31 1998-03-31 1998-04-01 1998-04-01 1998-03-31 1998-04-22 1998-04-15 1998-04-09 1998-04-22 1998-04-22 1998-04-29 60/080334 60/080328 60/080327 60/080194 60/080165 60/081819 60/081229 60/080333

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APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084639
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                                                                                                                                                                                                                                                                                                                500 V----CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS
                                                                                                                                                                                                                                                                                                                                                                                           448 PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                                                                                                               612
                                                                                                                                                                                                                                        553
                                                                                                                                                                                                                                                                              161
                                         330 ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
             723 LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                       SQTIVFICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN
                                                                                                                                                                                                ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                        DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ
                                                                                                                                                                                                                                                                            DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                      VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
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                                                                                                                                                               EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
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                                                                                       -ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
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US-09-978-608A-169
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Best Local 9
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 9263091222
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CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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ORGANISM: Homo sapiens
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672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGEISN---ALQKVDVQLIPQD 722
                                   270 SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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                                                                                                             ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                    DQE-----DQVDPRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
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                                                                         EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHEYHEEDSHDYDVALLQLDHEVVR 671
                                                                                                                                                 DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALTADRWVITAAHCFQ 611
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Botstein, David
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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Best Local Similarity 33.1%;
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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215 ESKKLIVRIGEYDLRR-WE--KW--ELDLDIKEVFVHENYSKSTTDNDIALIHLAQPATL 269
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                                                            DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
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Stewart, Timothy A.
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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                                             PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
                                                                                                         PRIOR APPLICATION NUMBER: 60/077641 PRIOR PILING DATE: 1998-03-11
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077450
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                                                                                                                                                  PRIOR FILING DATE:
        FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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Hillan, Kenneth J
Kljavin, Ivar J.
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Filvaroff, Ellen
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Grimaldi, J. Christopher
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PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/081071
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FILING DATE: 1998-03-20
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/080327
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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APPLICATION NUMBER:
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FILING DATE: 1998-03-31
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FILING DATE: 1998-03-30
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER:
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
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PRIOR PILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-04-30
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
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PRIOR APPLICATION NUMBER: 60/083495
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR APPLICATION NUMBER: 60/083500
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                                                                OR APPLICATION NUMBER: 60/085579
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/082796
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
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         APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Baker Kevin P
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PRIOR FILING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFYHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
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                                                                                                                                                                                                                   Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao, Wei-Qiang
                                                                                                                                                                                                          Stewart,
                                                                                                                                                                                                                                                                                                                                 Kljavin,
                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J.
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker Kevin P.
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                                                                                                                                                                                           Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                       Hillan, Kenneth J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botstein, David
                                                                                                                                                                                                                                                                                                 Napier,
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                                                                                                                                                                                                                                                                                                                  vin, Ivar J.
Sophia S.
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                                                                                                                                                                                                                                                                                                                                                                    i, J. Christopher Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanspeter
                                                                                                                                                                                                                                                                                              Mary A.
                                                                                                                                                                                                          Timothy A.
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PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/077632
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FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/078936
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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                                     APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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     APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: FILING DATE: 1998-04
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
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APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/083496
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
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FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/084441
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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/083558
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                                                       APPLICATION NUMBER: 60/085339
PILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
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FILING DATE: 1998-05-07
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Best Local 9
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APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
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                                                                                                            330 BCSEVMSNMVSENMICAGILGDRQDACEGDSGGENVA-SFHGTWFLVGLVSWGEGCGLIH 388
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783 YFGVYTRITGVISWI 797
                                  389 NYGYYTKVSRYLDWI 403
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                                                                                                                                                       SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                                          SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN
                                                                                                                                                                                                                               EDSMASTVLWTVFLGKVWQNSRWPGBVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR
                                                                                                                                                                                                                                                                      ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVPVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                           DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ
                                                                                                                                                                                                                                                                                                                                                  DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                         20.2%;
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Pred. No. 2.5e-31;
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RESULT 106 US-09-978-564A-169 ; Sequence 169, Ap ; Publication No. ; GENERAL INFORMAT APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Ashkenazi, APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT PPLICANT: INFORMATION Fong, Wei-Kljavin, Ivar J. Kuo, Sophia S. Napier, Mary A. Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J Ferrara, Napoleon Filvaroff, Ellen Eaton, Dan Desnoyers, Luc Botstein, David Baker, Kevin P Goddard, Audrey Gerritsen, Mary E. Gerber, Hanspeter Application US/09978564A ŪS20030050241A1 Sherman -Qiang Avi

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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION UMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/077641
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APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/077649
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APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079786
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/079663
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APPLICATION N
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Shelton, David L.
Stewart, Timothy A.
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  NUMBER: 60/080328
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PRIOR APPLICATION NUMBER: 60/083742
PRIOR APPLICATION NUMBER: 60/084366
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/083559 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083500 PRIOR APPLICATION NUMBER: 60/083545 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083554 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/080333 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/081070 APPLICATION NUMBER: APPLICATION NUMBER: 60/081049 FILING DATE: 1998-04-08 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081955 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-22 FILING DATE: FILING DATE: FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558 FILING DATE: APPLICATION NUMBER: 60/083499 APPLICATION NUMBER: 60/083392 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 FILING DATE: 1998-04-2: APPLICATION NUMBER: 60/082568 APPLICATION NUMBER: 60/081819 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-27 APPLICATION NUMBER: 1998-04-09 1998-04-08 1998-04-08 1998-04-29 60/081229 60/081071 60/083336 60/084639

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APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07

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Sequence 169, Application US/09999833A Publication No. US20030054405A1
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APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
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FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085339
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YFGVYTRITGVISWI 797
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                                                                                                                                                                                                                                                                                                       NYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                            LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                                                                                                                                                                      ECSEVMSNMYSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 09/065250
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077641
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: 60/079689
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Grimaldi, J. C
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Desnoyers, Luc
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P

Baker Kevin P.

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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/091195
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/082569
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/078936
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Williams, P. Mickey
Wood, William I.
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Filvaroff, Ellen
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Stewart, Timothy A.
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Desnoyers, Luc
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Kuo, Sophia S.
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Hillan, Kenneth J
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PRIOR FILING DATE: 1998-04-08
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52; Mismatches 145;
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                                                        TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
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Shelton, David L.
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR APPLICATION NUMBER: 60/085580
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECSEVMSNMVSENMLCAGILGDRODACEGDSG3PMVA-SFHGTWFLVGLVSWGEGCGLLH 388
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Desnoyers, Luc
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                                                                                                           Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                    Filvaroff,
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                                                                                                                                                                                                                                                                                                                                                                                                              Baker Kevin P.
                                                      Paoni
                                                                        Pan, James;
                                                                                         Napier, Mary A.
                                                                                                                                              Hillan, Kenneth J
                                                                                                                                                              Gurney, Austin L.
                                                                                                                                                                                                                        Goddard, Audrey
                                                                                                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                   Sherman
                                                    Nicholas F.
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f, Ellen
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PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR PRICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION UNMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
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                    DR FILING DATE: 1998-04-01
DR APPLICATION NUMBER: 60/08033
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DR APPLICATION NUMBER: 60/080334
DR PILING DATE: 1998-04-01
DR APPLICATION NUMBER: 60/081070
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
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FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-13
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FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077791
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/081049
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PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-39
PRIOR PELLORITON NUMBER: 60/083742
PRIOR PELLING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/084414
PRIOR APPLICATION NUMBER: 60/084414
PRIOR PILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR PILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/083554
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FILING DATE: 1998-05-07
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

Botstein, David Desnoyers, Luc Baker Kevin P.

APPLICANT: APPLICANT: APPLICANT:

Ferrara, Na Filvaroff,

Napoleon f, Ellen

Eaton, Dan

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                                                                            LĊŚĖAYRYQVTPRMĹĊĀĠYRKGKKDĀĊQĠDŚĠĠPLVCKALSĠRWFĹĀĠĹVŚWĠLĠĊĠRPN 782
                                                                                                                                                         SAAVRPVCLP----ARSHFPEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
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                                                                                                                ECSEVMSNMVSENMICAGIIGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                             SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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YEGVYTRITGVISWI
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Pred. No. 2.5e-31;
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DR APPLICATION NUMBER: 60/083322 OR FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081817 FILING DATE: 1998-03-31 FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/085582
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          LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                     ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SPHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                           SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN
                                                                                                                                                                     EDSMASTYLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                                                                         ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                               PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                          SAAVRPVCLP---
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PlC6
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PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION UNMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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PRIOR APPLICATION NUMBER: 60/077450
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PRIOR FILING DATE: 1997-11-03
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                                                                       PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Botstein, David
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Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER:
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S 밁 Ş Matches 113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------Similarity PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEB Conservative CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552 52; Score 470; DB 10; pred. No. 2.5e-31; 2; Mismatches 145 145; Indels 54; Gaps -RDTE 112 160 18;

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; Sequence 169, Application US/09999830A
; Publication No. US20030077700A1
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APPLICANT: Baker Kevin P
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C70
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION UNMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
            PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Stewart, Timothy A.
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PRIOR APPLICATION NUMBER: 60/079664
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FILLING DATE: 1998-05-15
RAPPLICATION NUMBER: 60/085704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%; Score 470; DB 10; Similarity 33.1%; Pred. No. 2.5e-31;
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
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Williams, P. Mickey
Mood, William I.
WENTION: Secreted and Transmembrane Polypeptides and
WRNTION: Acids Encoding the Same
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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                                                                                                                                          Paoni, Nicholas F
                                                                                                                                                                     Napier, Mary A.
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                                                                                                                                                          James;
                                                                                                                                                                                       vin, Ivar J.
Sophia S.
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PRIOR APPLICATION NUMBER: 60/080328
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/081071
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/080327
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DR FILLING DATE: 1998-03-30
DR APPLICATION NUMBER: 60/079923
DR FILING DATE: 1998-03-30
DR APPLICATION NUMBER: 60/080105
DR FILLING DATE: 1998-03-31
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R APPLICATION NUMBER: 60/079656
R PILING DATE: 1998-03-26
R APPLICATION NUMBER: 60/079664
R FILING DATE: 1998-03-27
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/080165
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR APPLICATION NUMBER: 60/084637
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PRIOR APPLICATION NUMBER: 60/084640
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PRIOR APPLICATION NUMBER: 60/084598
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PRIOR APPLICATION NUMBER: 60/083499
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PRIOR APPLICATION NUMBER: 60/083545
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PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083500 PRIOR APPLICATION NUMBER: 60/081229 PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR PILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05 PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083322 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336 PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/081203 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 FILING DATE: 1998-04-1 APPLICATION NUMBER: 60 FILING DATE: 1998-04-1 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 FILING DATE: 1998-04-27 FILING DATE: APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 APPLICATION NUMBER: 60/081838 APPLICATION NUMBER: 60/081819 FILING DATE: 1998-04-1 APPLICATION NUMBER: FILING DATE: 1998-04-09 FILING DATE: 1998-04-09 1998-04-22 1998-04-2 1998-04-15 60/081952 60/081955

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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                                   APPLICANT:
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APPLICATION NUMBER: 60/085704
TTING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/085580
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APPLICATION NUMBER: 60/
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                                    Fong, Sucr....
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                 Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
                                                                                                                Eaton, Dan
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33.1%; Pred. No. 2.5e-31;
vative 52; Mismatches 145;
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CURRENT APPLICATION NUMBER: US/09/978,187B
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR ETILING DATE: 2001-07-30
PRIOR PRIOR PRIOR DATE: 1997-10-17
PRIOR PRIOR DATE: 1997-10-17
PRIOR PRIOR PRIOR TILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
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FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649
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FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
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FILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/078936
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APPLICATION
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-08
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                         FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/084366
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DR FILING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/085582

DR FILING DATE: 1998-05-15

DR APPLICATION NUMBER: 60/085700

DR FILING DATE: 1998-05-15

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FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/085573
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085580
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                                                               ECSEVMSNMYSENMLCAGILGDRODACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                       SQTIVPICLPDSGLAERELNQAGQETLYTGWGYHSSREKEAKHNRTFYLNFIKIPVVPHN 329
                                                                                                                                                     EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
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Pred. No. 2.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches 124; Conservative
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TYPE: PRT
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723 LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
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                                                                                                SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTEVLNFIKIPVVPHN 329
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Grimaldi, J. Christopher
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botstein, David
Desnoyers, Luc
                                 ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                  SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                    EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
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Shelton, David L.
Stewart, Timothy A.
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US-09-978-375A-169
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NUMBER OF SEQ ID NOS: 624
SEQ ID NO 169
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 802
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                                                                                                                                                                                                                                                                    113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                           448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                        553
                                                                                                                                                                                           161
                                                                                                                                                                                                                                    500 V-
                                  270 SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                                                                                                                58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi, Avi
                                                                                                                                                    DEEHCDCGLQGPSSRIVGGAVSSEGEWPWO-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                         DOE-----DOVDERLIDGKWIRRGDSFWOVVLLDSKKKLACGAVLIHESWVLIAAHCMD 214
                                                                         EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHBEDSHDYDVALLQLDHPVVR 671
                                                                                                              ESKKILVRIGEYDIRR-WE--KW--ELDIDIKEVFVHPNYSKSITDNDIALIHLAQPATI 269
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Grimaldi, J. Christopher
Gurney, Austin L.
Gurney, Kenneth J
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, P. Mickey Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei-Qiang
                                                                                                                                                                                                                                  CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKXPNPQCDGRPDCRDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Audrey
                                                                                                                                                                                                                                                                                                                                                                                                           20.2%; Score 470; DB 10; 33.1%; Pred. No. 2.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                           52; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 802;
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US-09-978-298A-169
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                                                                                                                                                        PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR PILLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
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               PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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                                                                                                                                        PRIOR APPLICATION NUMBER: 60/077791
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PRIOR APPLICATION NUMBER: 60/077450
FILING DATE:
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Gerritsen, Mar,
Goddard, Audrey
Goddard, Paul J.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, Williams I.
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Grimaldi,
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Filvaroff, Ellen
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Hillan, Kenneth J
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1998-03-20
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/080328
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PRIOR FILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/080105
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
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PRIOR APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-04-08
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    FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/082569
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napole
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PRIOR APPLICATION NUMBER: 60/08579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
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          Roy, Marga
                                                                                                 Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                    Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Eaton, Dan
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                                                                    Pan,
                                                                                 Napier, Mary A.
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                                                James;
i, Nicholas F.
                                Margaret Ann
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                                                                                                                                                                                                                                                                            Sherman
David L. Timothy
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52; Mismatches 145;
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APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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CURRENT FILING DATE: 2002-03-19
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PRIOR APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/079664
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084639
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/083500
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                                                                                                                                                                                                                                                                                                                              DQE-----DQVDPRLIDGKNTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD
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                                                                                                                                                                             SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                     ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHRNYSKSTTDNDIALLHLAQPATL 269
YFGVYTRITGVISWI
                                                                   LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN
                                                                                                    ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGBGCGLLH 388
                                                                                                                                             SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
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; Sequence 169, Application US/09978194A
; Publication No. US20030195333A1
; GENERAL INFORMATION:

Ashkenazi, Avi

Baker Kevin P.

APPLICANT:
APPLICANT:
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APPLICANT:

Botstein, David Desnoyers, Luc Eaton, Dan

APPLICANT:

Ferrara, Napoleon Filvaroff, Ellen

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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILLING DATE: 1998-03-11
PRIOR PILICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Pan, James;
APPLICANT: Pan, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2630P1C10
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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OR APPLICATION NUMBER: 60/078886
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OR APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/064249
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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Kuo, Sophia S.
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Wei-Qiang
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DR APPLICATION NUMBER: 60/083322
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FILING DATE: 1998.04-01
APPLICATION NUMBER: 60/080334
FILING DATE: 1998.04-01
APPLICATION NUMBER: 60/081070 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080107 FILING OATE: 1998-03-31 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: PILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080327 FILING DATE: APPLICATION NUMBER: 60/081071 APPLICATION NUMBER: 60/081049 FILING DATE: 1998-04-08 FILING DATE: 1998-04-08 FILING DATE: APPLICATION NUMBER: 60/ FILING OATE: 1998-04-23 APPLICATION NUMBER: 60/081817 APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 FILING DATE: ON NUMBER: 60/080194 NUMBER: 60/083500 1998-04-01 1998-03-31 1998-04-22 1998-03-31 60/080328 60/080165 60/082796

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                                                                                                                                                                                                                                                                                                                                                 448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCKATF-QCKEDS---TCISLPK 499
                                                                                                                                                                                                                                                                                                                                                                                    58
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                      ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH
                                                                             SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                             SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                              EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR
                                                                                                                                                                             ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                                                                 DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                                                PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                  20.2%; Score 470; DB 10; 33.1%; Pred. No. 2.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                  52;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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SAAVRPVCLP---
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Sequence 169, Application US/09999829A Publication No. US20030195344A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/999,829A
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 NYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                        58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
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Kliavin, Ivar J.
                                                                                                                                                                                                                                                                                                  VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                            PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                        ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL
                                                                                                                                                                                                               DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
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Filvaroff,
                                                                               DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASIQVRGRHICGGALIADRWVITAAHCFQ 611
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Grimaldi, J. Christopher
Gurney, Austin L.
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Gerritsen, Mary E.
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Ef, Ellen
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-ARSHFFEBGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                                                                                                                                                                                                                                                                                                           145;
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Publication No. US20030199435A1
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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C3
CURRENT APPLICATION UNMBER: US/09/978,299A
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077641
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066364
                                                                                                FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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            APPLICATION NUMBER: 60/078886 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078936
                                                               APPLICATION NUMBER: 60/078004 FILING DATE: 1998-03-13
FILING
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
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Desnoyers, Luc
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Baker Kevin P.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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1998-03-20
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                APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
                                               FILING DATE: 1998-04
APPLICATION NUMBER:
FILING DATE: 1998-04
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APPLICATION NUMBER: 60/082704
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FILING DATE: 1998-04-15
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 APPLICATION NUMBER:
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ERIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03 APPLICATION NUMBER: APPLICATION NUMBER: 60/079664 FILING DATE: 1998-03-27 APPLICATION NUMBER: FILING DATE: 1998-03 APPLICATION NUMBER: APPLICATION NUMBER: 60/079728 APPLICATION NUMBER: APPLICATION NUMBER: 60/079689 ON NUMBER: 60/079923 1998-03-3 1998-03-30 1998-03-30 1998-03-27 1998-03-27 1998-03-26 1998-03-27 1998-03-27 60/080105 60/079920 60/079786 60/079663

FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 APPLICATION NUMBER: APPLICATION NUMBER: 60/080194 60/080165 60/080107

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APPLICATION NUMBER: APPLICATION NUMBER: 1998-04-09 1998-04-08 1998-04-08 1998-04-08 60/081071 60/081195 60/081203

APPLICATION NUMBER: 60/081817 APPLICATION NUMBER: 60/081955 1998-04-09 1998-04-15 1998-04-15 60/081229

APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15 1998-04-15 60/081838 60/081819

APPLICATION NUMBER: 60/082569 1998-04-21 60/082568

1998-04-22 1998-04-22 60/082804 60/082700

60/082796

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Query Match 20.2%; Score 470; DB 10; Best Local Similarity 33.1%; Pred. No. 2.5e-31; Matches 124; Conservative 52; Mismatches 145;
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PRIOR APPLICATION NUMBER: 60/085700
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PRIOR APPLICATION NUMBER: 60/085689
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PRIOR APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/083558
FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/084639
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FILING DATE: 1998-05-05
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
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           FILE REFERENCE: P2630P1C13
CURRENT APPLICATION NUMBER: US/09/978,544A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-07-30
PRIOR PELICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P
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                                                                                                                                                                                                                                                                 APPLICANT: Roy, Margaret Ann
APPLICANT: Sheaton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams of Transmembrane Folypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER:
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Grimaldi, J. Christopher
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Gerritsen, Mary E
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Filvaroff, Ellen
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Hillan, Kenneth J
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Kuo, Sophia S.
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PRIOR APPLICATION NUMBER: 60/084627
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PRIOR PILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/084414
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DR PELICATION NUMBER: 60/083558

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DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083496
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083499
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083545 R APPLICATION N R FILING DATE: : R APPLICATION N APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084639 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 FILING DATE: 1998-0:
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US-09-978-665A-169
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ERIOR APPLICATION NUMBER: 60/08579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR APPLICATION NUMBER: 60/085573
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Publication No. US20030199437A1
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Botstein, David
Desnoyers, Luc
                                                                   Paoni,
                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                      Fong,
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
                                                                                                                    Napier,
                                                                                                                                     Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                                              James;
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Pred. No. 2.5e-31;
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PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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CURRENT FILING DATE: 2001-10-16
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077450
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ITILE OF INVENTION: Acids Encoding the Same
                             PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/079664
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PRIOR FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER:
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       APPLICATION NUMBER: 60/081070
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                          NUMBER: 60/080327
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083496
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                                                            LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN
                                                                                      ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH
                                                                                                                                               SQTIVPICLPDSGLAERELNOAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                        ESKKLLVRIGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL
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RESULT 126
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                                                                                              GENERAL INFORMATION:
                            APPLICANT:
APPLICANT:
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                         Desnoyers,
Eaton, Dan
 Ferrara, Na
Filvaroff,
                                         Botstein, David
Desnoyers, Luc
                                                                     Baker Kevin
f, Rapoleon
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
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PRIOR PILICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
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TITLE OF INVENTION: Accide Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/978,802A
CURRENT FILING DATE: 2001-10-16
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
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PRIOR APPLICATION NUMBER: 60/079663
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/078004
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APPLICATION NUMBER: 60/079923 FILING DATE: 1998-03-30
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Goddard, Audrey
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Williams, P. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy, Margaret Ann
Shelton, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan, James;
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Kuo, Sophia S.
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
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PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/082700
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PRIOR PILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
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PRIOR APPLICATION NUMBER: 60/081838
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PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-22
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  OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083545
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OR FILLING DATE: 1998-04-29
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OR APPLICATION NUMBER: 60/083559
OR APPLICATION NUMBER: 60/083550
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER:
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FILING DATE: 1998-05-06
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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PILING DATE: 1998-05-15
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FILING DATE: 1998-05-07
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                                      330 ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWPLVGLVSWGEGCGLLH 388
                                                                                                                                                             612 EDSMASTVIWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                                                                   215 ESKKLLVRIGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                              553 DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                                                                                                                                            500 V---
                                                                                                                                                                                                                                                                                                                                                                                                            448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
723 LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                                                                                                                   113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124;
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                                                                                                                    SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                                                   DQE-----DQVDPRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                             SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                            -CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552
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US-10-164-749A-169
                                                                            ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-164-749A-169
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                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR PRILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
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Query Match 20.2%; Score 470; DB 12; Best Local Similarity 33.1%; Pred. No. 2.5e-31; Matches 124; Conservative 52; Mismatches 145
                                                                                                                                                          SEQ ID NO 169
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C60
                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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                                                                                                                                          802
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Williams, P. Mickey
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Stewart, Timothy A.
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Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy, Margaret Ann
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                                         Length 802;
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52; Mismatches 145;

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US-09-999-831A-169
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                                  CURRENT APPLICATION NUMBER: US/09/999,831A
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 169
LENGTH: 802
                                                                                                                                         APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C68
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TYPE: PRT
ORGANISM: Homo sapiens
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth J
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Pilvaroff, Ellen
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                                                                                                                                                                                                                                                                                                         Nicholas F.
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US-10-013-917A-169
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Query Match 20.2*; Score 470; DB 12;
Best Local Similarity 33.1*; Pred. No. 2.5e-31;
Matches 124; Conservative 52; Mismatches 145;
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                                FILE REFERENCE: P2630P1C82
CURRENT APPLICATION NUMBER: US/10/013,917A
CURRENT FILING DATE: 2001-10-25
                                                                                                                    APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Prior Application removed - See File Wrapper or Palm
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Desnoyers, Luc
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Paoni, Nicholas F
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Best Local S
Matches 124
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SEQ ID NO 169
LENGTH: 802
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OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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              Shelton, David I.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                               Pong,
                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                    Gao,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker Kevin P.
Botstein, David
                                                                                                                                                    Napier, Mary A.
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Pilvaroff, Ellen
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                                                                                                                     Paoni,
                                                                                                                                                                 avin, Ivar J., Sophia S.
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                                                                                                    Margaret Ann
                                                                                                                                       James;
                                                                                                                                                                                                                                                                                                                                 Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                     Sherman
                                                                                                                     Nicholas F
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR PILING DATE: 1997-11-21
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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CURRENT APPLICATION NUMBER: US/09/999,834A
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077649
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PRIOR FILING DATE: 1998-03-10
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OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
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                                                       APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/081071
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PRIOR FILING DATE: 1998-04-29
PRIOR APELICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
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FILING DATE: 1998-04-15
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/082568
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FILING DATE: 1998-04-29
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                  FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/084414
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FILING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/085704
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783 YFGVYTRITGVISWI 797
                                       389 NYGVYTKVSRYLDWI 403
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                                                                          LĊŚĖĄYRYQVTPRMIĊĄĠYRKGKKĎĄĊQĠĎŚĠĠPLVCKĄLSĠRWFLĄGLVSWGLGCGRPN
                                                                                                            ECSEVNSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SEHGTWFLVGLVSWGEGCGLLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                                                                                                   SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                                       SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN
                                                                                                                                                                                                                                                                ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                     DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.2%; Score 470; DB 12; Length 802; 33.1%; Pred. No. 2.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145;
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RESULT 131
US-10-162-521A-169
                                                                                                                                                                        Sequence 169, Application US/10162521A Publication No. US20030211092A1
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               APPLICANT:
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APPLICANT:
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   APPLICANT:
                                                                                                                                            Ashkenazi,
Rong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                               Baker Kevin P.
                                                        Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                 Desnoyers, Luc
                                                                                     Eaton, Dan
                                                                                                                  Botstein, David
                                                                                                                                              AVI
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Goddard, Audrey

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CURRENT APPLICATION NUMBER: US/10/162,521A
CURRENT FILING DATE: 2002-11-29
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
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LENGTH: 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 92630P1C55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PAIM. NUMBER OF SEQ ID NOS: 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077641
OR FILING DATE: 1998-03-11
OR FILING DATE: 1998-03-11
OR FILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 Match 20.2%; Score 470; DB 12; Length 802; Local Similarity 33.1%; Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/077450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/077791
                                                                                                                                                                                                                                                                                                                                                                                                                    448
672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                                                          553
                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                  500
                                                                                                                                                                                                                                                                                                                                                                113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK-------RDTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSPLNCSLDNGGCTHYCLEE 112
                                                                                                                                                                                                                                                      DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                       DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                                                                                                                               V----CDGQPDCLNGSDBEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552
                                                                                                                                                                                                                                                                                                                                                                                                                       PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                              SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                     EDSMASTVIWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                   ESKKLLVRIGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches 145; Indels 54;
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US-10-145-016A-169
; ORGANISM: Homo sapiens US-10-145-016A-169
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
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                                                        Remaining Prior Application data removed - See File Wrapper or PAIM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 169
LENGTH: 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C52
CURRENT APPLICATION NUMBER: US/10/145,016A
CURRENT PILING DATE: 2001-10-18
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                                                                                                                                                                PRIOR FILING DATE: 1998-03-11 PRIOR APPLICATION NUMBER: 60/077791
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR FILING DATE: 2001-07-30
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                                                                                                                                            PRIOR FILING DATE: 1998-03-12
                                                                                                                                                                                                         PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.
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Hillan, Kenneth J
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimaldi,
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US-10-145-088A-169
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Best Local Similarity 33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 169, Application US/10145088A Publication No. US20030203434A1 GENERAL INFORMATION:
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                                                                                                                                           APPLICANT:
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APPLICANT: Baker Kevin P
          TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630F1C49
CURRENT APPLICATION NUMBER: US/10/145,088A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 2001-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            783 YEGVYTRITGVISWI 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 PCAS--ICCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEB 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
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                                                                                                                                                                             Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth J
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Godowski, Paul J.
Grimaldi, J. Christopher
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Botstein, David
                                                                                                                                        Williams, P. Mickey Wood, William I.
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                       Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                             Kljavin,
                                                                                                                                                                                                                                                            James;
i, Nicholas F.
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                                                                                                                                                                                                                                                                                                                          Sophia S.
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                                                                                                                                                                                                                                                                                                                                             Ivar J.
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US-10-145-092A-169 RESULT 134

Sequence 169, Application US/10145092A Publication No. US20030203435A1 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Botstein, David Eaton, Dan Desnoyers, Luc Baker Kevin P.

APPLICANT: APPLICANT: PPLICANT:

Filvaroff, Ellen Gao, Wei-Qiang

Sherman Napoleon

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PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
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LENGTH: 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 624
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PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 20.2%; Score 470; DB 12; Local Similarity 33.1%; Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                 723 LCSEAYRYQVTPRMLCAGYRXGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                330 ECSEVNSNMVSENNLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                    672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN----ALQKVDVQLIPQD
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783 YFGVYTRITGVISWI 797
                                                    389 NYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                     ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See Pile Wrapper or PALM. NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/077641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/077649
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                   270 SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                               215 ESKKLLVRIGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                 500 V----CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552
                                                                                                                                                                                                                                                                                               113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKKMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                             448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                                                                                                                                                                                                                                                                                                                                      58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                 EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                        DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                 DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
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Wood, William I
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Grimaldi, J. Christopher
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Williams, P. Mickey
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Shelton, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.2%; Score 470; DB 12; Length 802; 33.1%; Pred. No. 2.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
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US-10-145-129A-169
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Publication No. US20030203436A1
                     SEQ ID NO 169
LENGTH: 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: P2630PLCS1
CURRENT APPLICATION NUMBER: US/10/145,129A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT:
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                                                                 PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/077641
                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-03-1
                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/077649
                                                                                                                                                                                                          PRIOR FILING DATE: 1998-03-
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/077450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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ORGANISM: Homo sapiens

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C9 CURRENT APPLICATION NUMBER: US/10/165,038A CURRENT PILING DATE: 2002-10-10
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APPLICANT:
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                                                                                    Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                   Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
Kljavin, Ivar J.
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Grimaldi, J. Christopher
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                                                                                                                                                                                                Paoni,
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Botstein, David
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Gerritsen, Mary E.
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Filvaroff, Ellen
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US-10-165-353A-169

Sequence 169, Application US/10165353A Publication No. US20030203442A1 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: APPLICANT: APPLICANT:

Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen

APPLICANT: APPLICANT: APPLICANT:

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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-12

REMAINING Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624
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PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1998-03-1
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PRIOR APPLICATION NUMBER: 60/066364
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TYPE: PRT
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                                                                                723 LÓSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                         330 ECSEVMSNWYSENWICAGILGDRQDACEGDSGGPWVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                          672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                                                                                      270 SQTIVPICLEDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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783 YFGVYTRITGVISWI 797
                                           389 NYGVYTKVSRYLDWI 403
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LENGTH: 802
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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NUMBER OF SEQ ID NOS: 624
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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APPLICATION NUMBER: 60/077450
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FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/077649
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  612
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                                                                                                                                                                                  500 V----CDGQPDCLNGSDEEQCQEGV--PCGTFTPQCE-DRSCVKKPNPQCDGRPDCRDGS 552
                                                                                                                                                                                                                                                                       448 PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                                                                                                                                                                                                                          113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK--
                                                                                                                                                                                                                                                                                                                                                                  124; Conservative
                                                                                                                                                                                                                                                                                                                  58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                     DQB-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
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Shelton, David L.
Stewart, Timothy A.
EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                             ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                       DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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US-10-167-600-169
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CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-07-30
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APPLICANT: Ashkenazi, Avi
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 624
SBQ ID NO 169
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
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                                                          PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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Botstein, David
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Wood, William I.
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Hillan, Kenneth J
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b. US20030203443A1
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ms, P. Mickey
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f, Ellen
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; Sequence 169, Application US/10170481A
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Best Local Similarity
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              APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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FILE REFERENCE: P2630P1C53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEGVYTRITGVISWI 797
                                                                                                                                                                       Pan,
                                                                                                                                                                                                                                                                                                                                                                             Fong,
                                                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers, Luc
Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker Kevin P
                                                                                                   Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                      Hillan, Kenneth J
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                        Gurney,
                                                                                                                                                                                                                                                                                                              Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                               Gerber, Hanspeter
                                                                                                                                                       Paoni,
                                                                                                                                                                                         Napier,
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                                                                                                                                                                                                                                                                                                                                                               We1-Qiang
                                                                                                                                                                           James;
                                                                                                                                                                                                         Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                   Sherman
                                                                                                                                                       Nicholas F
                                                                                                                                                                                       Mary A.
                                                                                                                                                                                                                                                            Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 470; DB 12;
Pred. No. 2.5e-31;
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RESULT 140

US-10-172-039A-169

Sequence 169, Application US/10172039A Publication No. US20030203445A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc APPLICANT: Baton, Dan

Baker Kevin P. Botstein, David

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SEQ ID NO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.2%; Score 470; DB 12; Best Local Similarity 33.1%; Pred. No. 2.5e-31; Matches 124; Conservative 52; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/170,481A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/662250
PRIOR APPLICATION NUMBER: 60/662250
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PRIOR PELLICATION NUMBER: 60/064249
PRIOR FILLING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILLING DATE: 1997-11-13
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PRIOR
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
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                                       389 NYGYYTKVSRYLDWI 403
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  783 YFGVYTRITGVISWI 797
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                                                                                                                                                                                                                                                                                                                                  ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                                                                                            DOE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                 LÓSEAYRYQVTPRMLCAGYRKGKKDÁCQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                         SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                   EDSMASTVÍMTVEÍGKVMQNSRWÞGEVSFKVSRLILHÞYHEEDSHDYDVÁLÍQÍÐHÞVVR 671
                                                                                                                                                                    SAAVRPVCLP-
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                                                                                                                                                                      -ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
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US-10-172-039A-169
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SEQ ID NO 169
LENGTH: 802
TYPE: PRI
                                                                                                                                                                                                                                                                                                                             Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT:
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/077641
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                                                               553 DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
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                                                                                                                                                                                                                                        448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
                      215 ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                             113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK-------RDTE 160
                                                                                                                                                                                                                                                                                 58 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSPLNCSLDNGGCTHYCLEE 112
                                                                                                      DOE-----DOVDERLIDGKWIRRGDSFWQVV/LLDSKKKLACGAVLIHESWVLTAAHCMD 214
                                                                                                                                                    V----CDGQPDCINGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-11-21
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APPLICANT: Williams, P. Mickey
APPLICANT: Wol, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C52
CURRENT APPLICATION NUMBER: US/10/210,028
CURRENT FILING DATE: 2001.10-18
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                                                                                                        PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 2001-07-30
                                             PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
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PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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Application data removed - See File Wrapper or PALM
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Eaton, Dan
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Local Similarity 33.1%;
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                                                                                                                                                                             Gurney, Australian, Kenneth J
Hillan, Kenneth J
Kliavin, Ivar J
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                                                Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Botstein, David
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Gerritsen, Mary E.
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Filvaroff, Ellen
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                  williams, P. Mickey
Wood, William I.
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; Pred. No. 2.5e-31;
52; Mismatches 145; Indels 5
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NUMBER OF SEQ ID NOS: 624
SEQ ID NO 169
LENGTH: 802
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Best Local (
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  783 YFĞVYTRITGVISWI 797
                                          389 NYGVYTKVSRYLDWI 403
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RESULT 143
US-10-167-749-169
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Botstein, David
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Godowski, Paul J.
Grimaldi, J. Christopher
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Gerritsen, Mary E.
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                                                                                           Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
Shelton, David L.
                                        Pan, James;
                                                  Napier, Mary A.
                                                              Kuo, Sophia S.
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                          Nicholas F
                                                                               Ivar J.
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Stewart, Timothy A.

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RESULT 144
US-10-013-921A-169
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
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CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
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NUMBER OF SEQ ID NOS: 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 802
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/062250
APPLICATION NUMBER: 60/064249
APPLICATION NUMBER: 60/064249
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FILING DATE: 1997-11-13
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                                                                                                                                                                                                                                                                                                                                                                    612
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                                                                                                                                                                                                                           330 ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                      :||||::: : ||
783 YFGVYTRITGVISWI 797
                                                                                                                                    389 NYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 20.2%; Score 470; DB 14; Similarity 33.1%; Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                    EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                  LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                        SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                                                                                                                                                                      SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
                                                                                                                                                                                                                                                                                                                                                                                                             ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
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Williams, P. Mickey
Wood, William I.
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Publication No. US20030068648A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-11
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FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/079663
                 APPLICATION NUMBER: 60/079689 PILING DATE: 1998-03-27
                                                APPLICATION NUMBER: 60/079664 PILING DATE: 1998-03-27
                                                                                APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26
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Williams, P. Mickey
Wood, William I.
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Hillan, Kenneth J
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Stewart, Timothy A.
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PRIOR
                                                 APPLICATION NUMBER: 60/083392
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-04-09
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NUMBER: 60/083499
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PRIOR APPLICATION NUMBER: 60/084640
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PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/084627
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APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/085704
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Similarity 33.1%; Pred. No. 2.5e-31;
24; Conservative 52; Mismatches 1455
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EDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVR 671
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448 PCPGEFICSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCTSLPK 499 PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112 ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269 DEEHCDCGLQGPSSRIVGGAVSSEGEWFWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611 VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160 -CDGQPDCLNGSDBEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS -DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214 Indels 54; Gaps 552

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PRIOR APPLICATION NUMBER: 60/064249
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PRIOR PILING DATE: 1997-11-33
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR PILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077631
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2630P1C89
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APPLICANT: Baker Kevin P
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Hillan, Kenneth J
Kljavin, Ivar J.
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Gao, Wei-Qiang
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Godowski, Paul J.
Grimaldi, J. Christopher
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Stewart, Timothy A.
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Filvaroff, Ellen
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o. US20030072745A1
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                   APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
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FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/080328
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Query Match
Best Local Similarity
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                                                    APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/083392
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Score 470; DB 14;
Pred. No. 2.5e-31;
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                                  SEQ ID NO 169
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                                                   Prior application removed NUMBER OF SEQ ID NOS: 624
                                                                                                     FILE REFERENCE: P2630P1C90
CURRENT APPLICATION NUMBER: US/10/016,177A
                                                                                       CURRENT FILING DATE: 2002-04-30
                                                                                                                                           TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALOKVDVQLIPQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 V----CDGQPDCLNGSDEEQCQEGV--PCGTFTFQCE-DRSCVKKPNPQCDGRPDCRDGS 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
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                                                                                                                                                                                                                                                                                                                                                                                              Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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                                                                                                                                                                               Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                 Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                            Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen, Mary E. Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botstein, David
                                                                                                                                                                                                                                                                                         Paoni,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker Kevin P
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o. US20030073131A1
                                                                                                                                                                                                                                                                                                        James;
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                                                                                                                                                                                                                                                                                           Nicholas F.
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                                                                    See File Wrapper or Palm
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US-10-016-177A-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 169, Application US/10166709A
Publication No. US20030104536A1
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Best Local 9
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               TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C99 CURRENT APPLICATION NUMBER: US/10/166,709A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
   CURRENT FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAAVR PVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKHMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCPGEFLCSVNGLCVPACDGVK----DCPNGLDERNCVCRATF-QCKEDS---TCISLPK 499
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gao, Wei-Qiang
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                                                                                         Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                               Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                      Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleon Filvaroff, Ellen
                                                                                                                                                                                                           Paoni,
                                                                                                                                                                                                                             Pan, James;
                                                                                                                                                                                                                                             Napier, Mary A.
                                                                                                                                                                                                                                                                  Kuo, Sophia S.
                                                                                                                                                                                                                                                                                    Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botstein, David
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                                                                                                                                                                                                           Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                        Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%; Score 470; DB 14; 33.1%; Pred. No. 2.5e-31; ative 52; Mismatches 145;
2001-10-19
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FILING DATE: 2001-07-30
APPLICATION NUMBER: 60/062250
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FILING DATE: 1998-04-0
APPLICATION NUMBER: 60
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
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FILING DATE: 1997-11-21
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FILING DATE:
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                                                                                                                                                 APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER:
                             APPLICATION NUMBER: 60/081195
                                                                       APPLICATION NUMBER:
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FILING DATE: 1998-04-01
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60/080333 60/080328 60/080327 60/080194 60/080165 60/080107

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             APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
                                                                   APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/084441
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FILING DATE: 1998-04-22
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FILING DATE: 1998-04-22
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RESULT 148 US-10-143-031A-169

Sequence 169, Application US/10143031A Publication No. US20030138439A1 GENERAL INFORMATION:

APPLICANT:

Eaton,

Dan

Desnoyers, Luc Botstein, David

APPLICANT:

Filvaroff, Ellen

APPLICANT:

Gao

Wei-Qiang Sherman

Fong,

APPLICANT: APPLICANT:

APPLICANT

APPLICANT: APPLICANT:

Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L.

APPLICANT:

APPLICANT: Ashkenazi, Avi

Baker Kevin P.

APPLICANT:

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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
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783
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                                                                              LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPN 782
                                                                                                                                                                                                                                                                                                                                   DEEHCDCGLQGPSSRIVGGAVSSEGEWPWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
YFGVYTRITGVISWI 797
                                     NYGVYTKVSRYLDWI 403
                                                                                                                        ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPNVA-SFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                                                                                                                                                                                                DQE-----DQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------RDTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCAS -- LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                                                  SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                                                           SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRURTFVLNFIKIPVVPHN
                                                                                                                                                                                                                                                   EDSMASTVIWTVFIGKVWQNGRWPGEVSFKVGRILLHPYHEEDSHDYDVALLQLDHPVVR
                                                                                                                                                                                                                                                                                             ESKKLLVRIGEYDIRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I, P. Milliam I, P. Milliam I, P. Milliam I TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C39
CURRENT APPLICATION NUMBER: US/10/143,031A
CURRENT PILING DATE: 2002-10-10
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PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-10
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CRGANISM: Homo sapiens
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723 LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGSPLVCKALSGRWFLAGLVSWGLGCGRPN
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                                        ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH
                                                                                    SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
                                                                                                                                                                              EDSMASTVLWIVELGKVWQNSRWPGEVSFKVSRLLLHFYHEEDSHDYDVALLQLDHPVVR 671
                                                                                                                                                                                                                      ESKKLLVRLGEYDLRR-WE--KW--ELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL 269
                                                                                                                                                                                                                                                                   DEEHCDCGLQGPSSRIVGGAVSSEGEWFWQ-ASLQVRGRHICGGALIADRWVITAAHCFQ 611
                                                                                                                                                                                                                                                                                                                DQE-----DQVDPRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
                                                                                                                                                                                                                                                                                                                                                                                                         VGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCAS--LCCGHGTCI---DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE 112
                                                                                                                                 SQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHN 329
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Shelton, David L.
Stewart, Timothy A.
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Kljavin, Ivar J.
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US-10-143-030A-169
; ORGANISM: Homo sapiens US-10-143-030A-169
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Publication No. US20
GENERAL INFORMATION:
                                                                 SEQ ID NO 169
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: P2630F1C33
CURRENT APPLICATION NUMBER: US/10/143,030A
CURRENT FILING DATE: 2002-08-27
                                                                                 Remaining Prior Application data removed - See Pile Wrapper or PALM NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR PILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/064249
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                    PRIOR PILING DATE: 1998-03-12
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                                                 LENGTH: 802
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/
FILING DATE: 1998-03-11
                                                                                                                                  FILING DATE: 1998-03-1
APPLICATION NUMBER: 6
                                                                                                                                                                    APPLICATION NUMBER: 60/077649
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Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shelton, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ran,
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Hillan, Kenneth J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
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5. US20030147901A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mary A.
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                                                                                                                                    60/077791
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Query Match 20.2%; Score 470; DB 14; Best Local Similarity 33.1%; Pred. No. 2.5e-31; Matches 124; Conservative 52; Mismatches 145;

Length 802; Indels

54;

Gaps

18;

1998-03-

1998-03-1

1998-03-20

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C72
CURRENT APPLICATION UNMBER: US/10/002,967A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
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APPLICANT: Ashkenaz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fong,
                                                                                                                                                                                                                                                                                Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                      James
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                                                                                                                                                                                                                                                               Daniel
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
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PRIOR FILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/081195
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PRIOR FILING DATE: 1998-03-27
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OR PILLING DATE: 1997-11-13
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FILING DATE: 1998-03-26
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FILING DATE: 1998-03-25
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PILING DATE: 1998-03-13
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PILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/080334
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                             NYGVYTKVSRYLDWI
                                                                               ECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVA-SFHGTWFLVGLVSWGEGCGLLH 388
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YFGVYTRITGVISWI
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                                                                                                                                                                                                                                                                             DQB-----DQVDPRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMD 214
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                                                                                                                        SAAVRPVCLP----ARSHFFEPGLHCWITGWG--ALREGGPISN---ALQKVDVQLIPQD
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                                                          LCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGFLVCKALSGRWFLAGLVSWGLGCGRPN
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Copyright (c) 1993 - 2004 Compugen Ltd.
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         US-08-295-411-1
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US-09-657-570A-3
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US-10-182-263-1
PCT-US92-10242-1
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5460953-3
US-08-756-506-2
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RESULT 1
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Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
                                                                                                                                          TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
             STREET: 10666 N
CITY: La Jolla
STATE: CA
                                               ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
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SEQUENCE CHARACTERISTICS:
LENGTH: 419 amin
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Best Local Similarity 100
Matches 419; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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LOCATION:
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LOCATION: 170.41
OTHER INFORMATION:
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Pred. No. 8.7e-191;
0; Mismatches 0;
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                                                                                                                        Matches
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CORRESPONDENCE ADDRESS:
ANDRESSE: Office of Patent Counsel, The Scripps
ANDRESSEE: Office of Patent Counsel, The Scripps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: OTHER INFORMATION: I
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                             Similarity
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Rolf M.
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Peptide"
                                                                                                                                                                                                                                                       /note= "Protein C Heavy Chain
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                                                                                                            Score 2324; DB 2; Length 419;
Pred. No. 8.7e-191;
Nismatches 0; Indels 0
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CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION UNMBER: 60/045,255
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID MOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID MO 3
LENGTH: 419
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APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein
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Huang, Lihua
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Sequence 1, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serine Protea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION UNUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gerlitz, Bruce E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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OTHER INFORMATION: /:
OTHER INFORMATION: /:
FEATURE:
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INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO
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ANTI-SENSE: N
FEATURE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION:
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LOCATION:
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                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCNDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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US-10-182-263-2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                             KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                     SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 402
                                                                                                                                                     KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
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Patent No. 5225537

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APPLICANT: GERLITZ, BRUCE E.; GRINNELL, ERIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
GLYCOSYLATION MUTANTS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID;
PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/07/459,082
FILING DATE: 29-DEC-1989
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                                                                                                                                                               Matches
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                                                                                                                                                                                                      Query Match
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FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 628,063
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                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-DEC-1990
APPLICATION NUMBER: 484,081
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                                                                                                                                                                                                                                                                                LENGTH: 461
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                                                                                                                                                        tch 99.7%; Score 2318; DB 6; al Similarity 99.8%; Pred. No. 3.2e-190; 418; Conservative 0; Mismatches 1;
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61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLWCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                       43 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLBHPCA 102
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100.0%; Pred. No. 9.
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    Mismatches

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9.8e-191;
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RESULT 9
US-08-756-506-2
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                                                                                 ; MOLECULE TYPE: protein US-08-756-506-2
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  Query Match
Best Local Similarity
Matches 418; Conserva
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                                                                                                                                                                                            TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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CITY: Seattle
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                                                                                                                                                       LENGTH:
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1201 Eastlake Avenue East
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    Conservative
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99.7%; Score 2317; DB 2; Length 460; 100.0%; Pred. No. 3.9e-190; tive 0; Mismatches 0; Indels
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US-08-756-506-4
; TOPOLOGY: li; MOLECULE TYPE: US-08-756-506-4
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                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Temperiey, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Dona E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
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APPLICANT:
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
DEFERRATION NUMBER: 61.
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                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6672
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                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
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                                                         TYPE: amino acid
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                          TELEFAX:
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Best Local S
Matches 414
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APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
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                                                                                                                                                                                                                                                                                                                             SEQ ID NO 5
LENGTH: 4:
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                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                            121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVFPRLIKGKWTRRGD
                                                                       SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                           Conservative
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5270178-18
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;Patent No. 5270178
;APPLICANT: GERLITZ, BRUCE E.,GRINNELL, BRITTILE OF INVENTION: VECTORS AND COMPOUNDS
;ZYMCGEN FORMS OF HUMAN PROTEIN C
;NUMBER OF SEQUENCES: 21
;CURRENT APPLICATION DATA;
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APPLICATION NUMBER:

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BRIAN W.

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; APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRI
; TITLE OF INVENTION: VECTORS AND COMPOUNDS
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NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/484,133
FILING DATE: 23-FEB-1990
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Similarity 98.6%;
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Pred. No. 5.3e-188;
3; Mismatches 3;
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NDS FOR EXPRESSION
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US-10-182-263-3
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APPLICANT: Gerlitz, Bruce E
                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10182263 Patent No. 6630138
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                             TYPE: PRI
ORGANISM: Homo sapiens
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O NO:18:
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                                                                      ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
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Pred. No. 7e-188;
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Pred. No. 5.3e-188;
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; TYPE: PRT
; ORGANISM: Homo &
US-10-182-263-6
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US-10-182-263-6
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Best Local Similarity
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APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
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CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION WIMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
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TITLE OF INVENTION: VECTORS AND COMPOUNDS
; ZYMOGEN FORMS OF HUMAN EROTEIN C
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/484,133
                        S
                                                                                                                                     5270178-14
                                                                                                                                                                                                                                                                                        ;Patent No. 5270178
; APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
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                                                                                                                                                                                                             ZYMOGEN FORMS OF HUMAN PROTEIN C
, NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA;
, APPLICATION NUMBER: US/07/
                                                                                                                                                                           SEQ ID NO:14:
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                                                            Best Local Similarity 98.6
Matches 413; Conservative
                                                                                                Query Match
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Pred. No. 1.6e
                                                          Score 2286.5; DB 6;
Pred. No. 1.6e-187;
3; Mismatches 2;
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APPLICANT: Grinnell, Brian W
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION UNMER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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LENGTH: 419
TYPE: PRT
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APPLICANT: Gerlitz, Bruce
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Patent No. 6630138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNVGVYTHVSRYLDWIHGHIRDKEAPQKSWAP 460
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                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKKMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                            ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAPWSKHVDGDQCLVLFLEHPCA 60
                                                                                                SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWBKWELDLDI 240
                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVFPRLIKGKWTRRGD
                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                              SPWQVVLLDSKKKSACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
    98.4%;
98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 2286; DB 4;
Pred. No. 1.5e-187;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 419;
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US-09-065-872-1
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US-09-667-570A-1
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GENERAL INCORMATION:
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein
FILE REFERENCE: aPC process patent
CURRENT APPLICATION NUMBER: US/09/065,872
CURRENT FILING DATE: 1998-04-24
EARLIER FILING DATE: 1997-04-28
RUMBER OF SEQ ID NOS: 2
RUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09065872
Patent No. 6162629
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Sequence 1, Application US/09667570A
Patent No. 6436397
GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                               AKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFH 369
                                                                                                                                                                                                                                                                                                    SKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKE
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; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-570A-1
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; APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMFOUNDS FOR E.
; TITLE OF INVENTION PROTEIN C
;ZYMOGEN FORMS OF HUMAN PROTEIN C
;NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/484,133
; FILING DATE: 23-FEB-1990
; TILING DATE: 23-FEB-1990
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PRIOR FILING DATE: 2000-9-21
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 3
SOPTMARE: Pare----
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TITLE OF INVENTION: Improved Methods for Processing Activated Protein
FILE REPERENCE: X-11796A
CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
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APPLICANT:
APPLICANT:
                                                                                                               Best Local Similarity
                                                                                                                                       Query Match
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42 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFTSKHVDGDQCLVLPLGHPCA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLABERELNQAGQETLVTGWGYHSSREKE 309
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                           ANSFLEBURHSSIERBCIEBICDFBEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLBHPCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.1%; Score 2281; DB 4; Length 410; illarity 100.0%; Pred. No. 4e-187; Conservative 0; Mismatches 0; Indels
                                                                                                Conservative
                                                                                                                 98.1%;
99.0%;
                                                                                           Score 2279.5; DB 6; Pred. No. 6.3e-187; 0; Mismatches 3;
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                                                                                                                                            DB 6;
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                                                                                                                                            Length 461;
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61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120

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GENERAL INFORMATION:

-09-065-872-2

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APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein
FILE REFERENCE: aPC process patent
CURRENT APPLICATION NUMBER: U$/09/065,872
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: 60/045,255
EARLIER APPLICATION NUMBER: 60/045,255
EARLIER FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 2, Application US/09065872
Patent No. 6162629
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APPLICANT: Carlson, Andrew D
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Local Similarity 100.0%;
311 KRNRTFVLNFIKIPVVFHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHG 370
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                                                                        APPLICANT: GERLITZ, BRUCE B.; GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
ZYMOGEN FORMS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                   ;Patent No. 5270178
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APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein
FILE REFERENCE: X-11796A
CURRENT APPLICATION NUMBERS: US/09/667,570A
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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PRIOR APPLICATION NUMBER: 60/045,255
PRIOR PILING DATE: 1997-04-28
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ORGANISM: Homo sapiens
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  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 23-FEB-1990
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; ORGANISM: Homo sapiens US-09-065-872-2

LENGTH: 409 TYPE: PRT

Query Match

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5270178-16
5270178-16
PRECENT: NO. 5270178
APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
ZYMOGEN FORMS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 21
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                          Matches 407;
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241 KEVFYHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                            ŚPWQVVLLDŚKKKLACGAVLIHPŚWVLTAAHCMDEŚKKLIVRIGEYDLRRWEKWELDLDI 281
                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKKSHLKRDTEDQEDPVFPRL-NGKMTRRGD
                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                         ANSFLEELRHSSLERBCIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPMVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYHSSREKEAKRNRIFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVRVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEVPVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGPMVASFHGTWFLVGLVSWGEGCGLLHNVGVYTHVSRYLDWIHGHIRDKEAPQKSWAP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVNSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                        96.6%;
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    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                      Score 2244.5; DB 6; Pred. No. 6.1e-184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2271.5; DB Pred. No. 3e-186;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 460;
                                                                                                                                                                                                                                                                                                                                                                      7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 460;
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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US-07-720-189-1
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                                                                                                                                        Matches 262;
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/07720189
Patent No. 5279956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: APC POLY.
TITLE OF INVENTION: APC, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19910724
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3366 No
CITY: La Jolla
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bingham, Doug
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UPFILING DATE: 19910724
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: The Sci
ADDRESSEE: Counsel
                                                                                              158 DTEDQEDQVDPRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK 217
                    218 KLLVRLGBYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402
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                                                           1 DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK 60
                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
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3366 No. 5279956th Torrey Pines Court, Suite 240
                                                                                                                                                                                                                                                                                                                                                                                                                                  262 amino acids
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                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                              Region
1..262
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                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Douglas
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ANTIBODIES, DIAGNOSTIC METHODS AND SYSTEMS FOR INHIBITING
APC, AND THERAPEUTIC METHODS
11
                                                                                                                                                        61.1%; Score 1419; DB 1; 100.0%; Pred. No. 1.2e-113;
                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                  /note= "In SEQ ID NO 1 is the sequence for
the PC heavy chain, the amino acid residue
which begin at position 158 and end at 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/720,189
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                                                                                                                                        Mismatches
                                                                                                                                                                             DB 1; Length 262;
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5270178-20
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                                                                                                                                                         ;SEQ ID NO:20:
LENGTH: 261
                                                                                                                                                                                                      APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.

ZYNGEN FORMS OF HUMANN PROTEIN C

NUMBER OF SEQUENCES: 21

CURRENT APPLICATION UNMBER. US/07/484,133

FILING DATE: 23-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5270178-19
                                                                                                                                                                                                                                                                                                                                                        Patent No. 5270178
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NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/484,133
FILING DATE: 23-FEB-1990
                                                        Matches 258;
                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
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APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Local sime
thes 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 261
158 DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 RYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 MVSENNICAGIIGDRQDACEGDSGGPMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 MYSENMICAGILGDRQDACEGDSGGPMYASFHGTWFLVGLYSWGEGCGLLHNYGVYTKVS 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSBVMSN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHQMDESK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRURTFVLNEIKIPVVPHNECSEVMSN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 KLLVRIGEYDLRRWEKWELDLDIKEVFVHDNYSKSTTDNDIALLHIAQPATISQTIVFIC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 RYLDWIHGHIRDKEAPOKSWAP 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFTKIPVVPHNECSEVMSN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC 120
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Similarity 98.9%;
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                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                          59.6%; Score 1384.5; DB 6; Length 261; 98.5%; Pred. No. 1.1e-110; ative 1; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                          Gaps
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                      US-08-944-483-51
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US-08-944-483-51
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GENERAL INFORMATION:
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                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acid
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                              STRANDEDNESS:
                                                                                                         TYPE:
                                                               TOPOLOGY:
                                                                                                                                                                                               TELEX:
                                                                                                                                                                                                                 TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                  NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN 179
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                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08944483
                                                                                                                       250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Abbott Park Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLASS, MICHAEL R.
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                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                          No. 6232456e
                                                                                 single
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RESULT 31
5270178-5
5270178-5
;Patent No. 5270178
; APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W.
; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
;ZYMOGEN FORMS OF HUMAN PROTEIN C
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5270178-21
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TITLE OF INVENTION: VECTORS F.ZYMOGEN FORMS OF HUMAN PROTEIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.3%; Score 1354; DB 3; Length 250; Best Local Similarity 100.0%; Pred. No. 4.2e-108; Matches 250; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/484,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 LIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLR 229
                                                                                                                                                                                                                                                                                                  398 RYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                 180 MVSENMLCAĞİLĞDRQDACEGDSGGPMVASFHGTWFLVĞLVSWGEGCĞLLHNYGVYTKVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTELHKLQTYPR-TNGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEAPQKSWAP 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRUCE E.; GRINNELL, BRIAN W. VECTORS AND COMPOUNDS FOR E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.9%; Score 1346.5; DB 6; Length 261; 96.2%; Pred. No. 1.9e-107;
US/07/484,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOR EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
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Best Local Similarity
Matches 249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
PILING DATE: Pebruary 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 22
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                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                           LENGTH: 487 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                      617 542 8906
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95.0%;
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                                                                              53:
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Pred. No. 6.6e-105;
0; Mismatches 12;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The gersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
APPLICANT: Etzerodt, Michael
APPLICANT: TIVENTION: IMPROVED METHOD FOR THE REFOLDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.8%; Score 809.5; DB 1; Length 487; Best Local Similarity 36.8%; Pred. No. 3.4e-61; Matches 172; Conservative 72; Mismatches 150; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/08469658 Patent No. 5917018
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                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
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                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
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     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                    USA
February 4, 1994
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Pred. No. 3.4e-61;
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NAME: Paul T. Clark
REGISTRATION NUMBER: 30,:
REPERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617 542 5070
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TYPE: amino acid
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                                               384 CGLLHNYGYYTKYSRYLDWI------HGHIRDKEAPQKSW 417
                                                                                                 382 PYVDRSTCKLSSSFTITENMFCAGYDTQPEDACQGDSGGPHVTRFKDTYFVTGIVSWGBG 441
                                                                                                                                              324 PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG
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CARKGKFGVYTKVSNFLKWIDKIMKARAGAAGSRGH---SEAP-ATW 484
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RESULT 34
US-08-469-486-2
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                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Thosesesen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 58
                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                        STATE: Massachusetts
                                                      CITY: Boston
                                                                              STREET:
                      COUNTRY:
02110-2804
                                                                                 225 Franklin Street
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RESULT 35
US-08-469-658-2
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                 Sequence 2, Application US/08469658 Patent No. 5917018 GENERAL INFORMATION:
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Best Local Similarity 36.8
Matches 172; Conservative
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEPAX: 617 542 8906
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 492 amino acid
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REGISTRATTORNE: Paul T. Clark
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APPLICATION NUMBER: US/08/469,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ---REVSFLNCSLDNGGCTHYCLEEVGWRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ANSFLEEVKQGNLERECLEEACSLEEAREVFEDAEQTDEFWSKYKDGDQC----EGHPCL 96
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                                                                                                                                                                 CARKGKFGVYTKVSNFLKWIDKIMKARAGAAGSRGH---SEAP-ATW 484
                                                                                                                                                                                                         CGLLHNYGVYTKVSRYLDWI------HGHIRDKEAPQKSW 417
                                                                                                                                                                                                                                                    PYVDRSTCKLSSSFTITPNMFCAGYDTQPEDACQGDSGGPHVTRPKDTYFVTGIVSWGEG
                                                                                                                                                                                                                                                                                            PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG
                                                                                                                                                                                                                                                                                                                                       TPIRFRRNVAPACLPEKDWAEATL--MTQKTGIVSGFG-----RTHEKGRLSSTLKMLEV 381
                                                                                                                                                                                                                                                                                                                                                                                 QPATISQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                         YVLTAAHCLHQAKRFTVRVGDRNTEQBEGNEMAHEVEMTVKHSRFVKETYDFDIAVLRLK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKBVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSIDLIGINRTEPSAGEDGSQVVRIVGGRDCAEGECPWQALLVNEENEGFCGGTILNEF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSCAHGYVLGDDSKSCVSTERFPCGKFTQGRSRRWAIHTSEDALDASELEHYDPADLSPT 208
Th egersen, Hans Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.8%; Score 809.5; DB 1; Length 492; 36.8%; Pred. No. 3.5e-61; stive 72; Mismatches 150; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RLIDGKMTRRGDSPWQVVILDSKKKLACGAVLIHPS 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMERE: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,658 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IMPROVED TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Holtet, APPLICANT: Etzerod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 492 amino acids
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                                                                                                                                                                                                                                                                                                                   149
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                   324 PVVPHNECSEVMSNMVSENNLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGBG 383
                                                                                                                                                                                   205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTIDNDIALLHLA 264
                                                                                                                                                                                                                             209 ESSLDLLGLNRTEPSAGEDGSQVVRIVGGRDCAEGECPWQALLVNBENEGFCGGTILNEF 268
                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ---REVSFLNCSLDNGGCTHYCLEEVGWRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFLEEVKQGNLERECLEEACSLEEAREVFEDAEQTDEFWSKYKDGDQC----EGHPCL 96
                                                             TPIRFRRNVAPACLPEKDWAEATL--MTQKTGIVSGFG-----RTHEKGRLSSTLKMLEV
                                                                                                  QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKBAKRNRTFVLNFIKI 323
                                                                                                                                            YVLTAAHCLHQAKRFTVRVGDRNTEQEEGNEMAHEVEMTVKHSRFVKETYDFDIAVLRLK 328
                                                                                                                                                                                                                                                                                                              CSCAHGYVLGDDSKSCVSTERFPCGKFTQGRSRRWAIHTSEDALDASELEHYDPADLSPT 208
                                                                                                                                                                                                                                                                                                                                                      CSCAPGYKLGDDLLQCHPAVKFPCGR-PWKRMBKKRSHLKRDTED--QEDQVDP----- 168
                                                                                                                                                                                                                                                                                                                                                                                                  N----QGHCKDGIGDYTCTCAEGFEGKNCEFSTREI----CSLDNGGCDQFCREERSEVR 148
                                                                                                                                                                                                                                                                  -----RLIDGKWTRRGDSPWQVVLLDSKKKCLACGAVLIHPS 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.8%; Score 809.5; DB 2; 36.8%; Pred. No. 3.5e-61; rative 72; Mismatches 150;
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Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 492;
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PCT-US92-10068-1
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PCT-US92-10068-1
                                Query Match 34.8%; Score 809; DB 5; Length 448; Best Local Similarity 35.7%; Pred. No. 3.4e-61; Matches 163; Conservative 87; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fitting, Thomas
REGISTRATION NUMBER: SCR1221P
REFERENCE/DOCKET NUMBER: 34,16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Factor X-Derived Polypeptides and TITLE OF INVENTION: Anti-Peptide Antibodies, Systems a NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                            NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /
OTHER INFORMATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Edgington, Thomas S
APPLICANT: Fair, Daryl S
TITLE OF INVENTION: Factor X-De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                      NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relaction
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CITY: L
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                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 448 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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1 ANSFLEBLRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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10666 North Torrey Pines Road
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                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                      /note= "Factor X Heavy Chain"
                                                                                                                                                                                          Tripeptide"
                                                                                                                                                                                                                                                                          /note= "Factor X Light Chain"
                                                                                                                                                                                                          /note= "Factor X Connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 07/798,221
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                                   56;
                                Gaps
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                TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
                                              CLASSIFICATION: 530
ATTORNSY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 10.
                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
COUNTRY: USA
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PILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION MATA:
APPLICATION NUMBER: US 07/793,989
PILING DATE: 18-NOV-1991
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APPLICANT: Mesters, Rolf M.

TITLE OF INVENTION: Serine Protease-Derived Polypeptides and

TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods

TITLE OF INVENTION: for Inhibiting Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGBG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 CARKGKYGIYTKVTAPLKWIDRSMKTRGLPKAKSHAP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED-------QVD 167
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TSRI263.0C1
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                                                                                                                                                                                                              Sequence 3, Application US/08955471 Patent No. 5968751 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.7%; Score 807; DB 1; Length 448; Best Local Similarity 35.4%; Pred. No. 5.1e-61; Matches 162; Conservative 88; Mismatches 151; Indels 56;
                                                      APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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LOCATION: 140..142
OTHER INFORMATION: /
OTHER INFORMATION: 7
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LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 PVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 TPITERMIVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 YILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                    CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVLTAAHCMDESKKLLVRIGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
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US-08-955-471-3
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INFORMATION FOR SEQ ID NO: 3:
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NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LOCATION: 140..142
OTHER INFORMATION: /
OTHER INFORMATION: T
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APPLICATION NUMBER: US/08/955,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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LOCATION: 143..448
OTHER INFORMATION:
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ZIP: 92037
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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STATE: CA
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                       265 QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                            205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                    55 -- CONOGRCKBGLGEYTCTCLEGFEGRNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 111
                                                                                                                                                                                                                                                                                                                                                                                 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED------QVD 167
                                                               YILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK 289
                                                                                                                                                      PTENPEDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 229
                                                                                                                                                                                                                                           ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 169
                                                                                                                                                                                                                                                                                                                                                                                                                           ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.7%; Score 807; DB 2; Length 448; 35.4%; Pred. No. 5.1e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Factor X Connecting
Tripeptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Mismatches 151; Indels
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RESULT 39
PCT-US92-10242-3
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GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serine Proteat
TITLE OF INVENTION: Anti-Peptide J
                      Query Match
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: SCIENCESCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
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                                                                                                                           FEATURE: Region
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                          NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 10666 North Torrey Pines Road, TPC 8 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                               LOCATION: 1..139
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fitting, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                  LOCATION: 143..44
                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 PVVPHNECSEVMSNMVSENNLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 TPITFRMNVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 342
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                                                                                                                                                                                                                                                                                                             Region
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                                                                                                        143..448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine Protease-Derived Polypeptides and Anti-Peptide Antibodies, Systems and Therapeutic Methods for Inhibiting Coagulation
34.7%;
                                                                                                                                                                        Tripeptide"
                                                                                                                                                                                                                                                                                   /note= "Factor X Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 07/793,989
                                                                                    /note= "Factor X Heavy Chain"
                                                                                                                                                                                             /note= "Factor X Connecting
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Score 807; DB 5; Length 448; Pred. No. 5.1e-61;
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US-09-367-777-44
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Patent No. 6562598
GENERAL INFORMATION:
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                                    APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlokat, Uwe
TITLE OF INVENTION: Factor X Deletion Mutants
and Analogues Thereof
                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Himmelspach, Michele Pfleiderer, Michael
                                                                                                                                                 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 PVVPHNBCSEVMSNYVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 YILTAAHCLYQAKREKVRVGDRNTEQBEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEXKRSHLKRDTEDQED------QVD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 -- CONOGRCKBGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLEELRHSSLERECIEEICDFEBAKEIFQNVDDTLAFWSKHVDGDQCLVLFLBHPCA 60
                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: CA
                                                                                                                                                                                             APPLICATION NUMBER: US/09/367,777 FILING DATE: 10-No. 6562598-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP
REGISTRATION NUMBER: 42,271
                    NAME: Ausenhus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09367777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Falkner, Falko-Guenter
Eibl, Johann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorner, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                               USA
                    Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPS 204
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RESULT 41
US-09-367-791A-27
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09367791A Patent No. 6573071 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
         COMPUTER READABLE FORM:
                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       TITLE OF INVENTION: Factor X Analogues With
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Himmelspach, Michele
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 TPITFRMNVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 APGYKLGDDLLQCHPAVKFPCGRPWKRNEKKRSHLKRDTEDQED-------QVD 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 -- CONOGRCKÓGLGEYTCTCLEGFEGKNCELPTRKL-CSLDNGDCDQFCHEEQNSVVCSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SICCGHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSIDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSP----- 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGES 442
                                                      COUNTRY: USA
                                                                                 STATE: CA
                                                                                                       CITY: San Francisco
                                                                                                                 STREET: Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 269
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                                  ZIP: 94111-3834
                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 488 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                      Dorner, Friedrich
Fisch, Andreas
                                                                                                                                                                                                                                                                                                                                  Schlokat,
                                                                                                                                                                                                                                                                  Johann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.6%; Score 803; DB 4; Length 488; 35.4%; Pred. No. 1.2e-60;
                                                                                                                                                                                                                 a Modified Protease Cleavage Site
                                                                                                                                                                                                                                                                                                                                         Uwe
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                                                                  RESULT 42
US-08-295-411-5
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                   Sequence 5, Application US/08295411 Patent No. 5679639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: AUSENDUS, Scott L.
REGISTRATION NUMBER: 42,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/267,791A
FILING DATE: 12-No. 6573071-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 20695D-000700US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                             384 CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                        383
                                                                                                                                                                                                                                                                                                       324
                                                                                                                                                                                                                                                                                                                                              330 TPITPRMNVAPACLPERDWARSTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                       270 YILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK 329
                                                                                                                                                             443 CARKGKYĞIYTKVTAFLKMIDRSMKTRGLPKAKSHAP 479
                                                                                                                                                                                                                                                                                                                                                                                        265 QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTIDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 P-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 -- CONOGECEDGEGETCTCLEGFEGENCELFTERL-CSLDNGDCDQFCHEEQNSVVCSC 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANSFLEBLRHSSLERECIEEICDEBEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
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                                                                                                                                                                                                                                                      PYVDRNSCKLSSSFIITQNMFCAGYDIKQEDACQGDSGGPHVIRFKDTYFVTGIVSWGES 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED------QVD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANSFLEEMKKGHLERECMEETCSYBEAREVFEDSDKTNEFWNKYKDGDQCETSP----- 94
                                                                                                                                                                                                                                                                                               PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 488 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FBB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-02
TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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LOCATION: 153..406
COTHER INFORMATION: /I
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33.7*; Score 783; DB 1; Length 400
Best Local Similarity 38.8*; Pred. No. 5.1e-59;
Matches 164; Conservative 76; Mismatches 147; Indels
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APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
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CORRESPONDENCE ADDRESS:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                119 SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPKLIDGKMTRR 178
236 LDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNOAGOET 295
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                                                                  GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                        SPCQNGGSCKDOLQSYICFCLPAFEGRNCETHKDDOLICVNENGGCEQYCSDHTGTKRSC 112
                                                                                                                                                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                                                                                                                                                                  ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC-----AS 52
                                        GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE
                                                                                                                      RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Factor VII Heavy Chain"
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US-08-955-471-5
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GENERAL INFORMATION:
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         FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine |
TITLE OF INVENTION: Anti-Per
                                                                                                                                                       ANTI-SENSE:
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                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                     LOCATION:
                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : La Jolla
E: CA
TRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                  Fitting, Thomas
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10666 No. 5968751th To
                                                                                                                                                                                                                                          406 amino acids
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                                                                                                     Region
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
in Inhibiting Coagulation
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            /note= "Factor VII Heavy Chain"
                                                                                 /note= "Factor VII Light Chain"
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34,163
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RESULT 44
PCT-US92-10242-5
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                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Seri-
TITLE OF INVENTION: Anti-
TITLE OF INVENTION: for
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                   APPLICATION NUMBER: US 07/793,989 FILING DATE: 18-NOV-1991 ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Griffin, John H.
                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 33.7%; Score 783; DB 2; Length 406; Local Similarity 38.8%; Pred. No. 5.1e-59; nes 164; Conservative 76; Mismatches 147; Indels 36;
                                                                                                                                                                                             FILING DATE:
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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Patent No. 5788965
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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LENGTH: 406 amino acid
                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
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NAME/KEY: Region
LOCATION: 1..152
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HYPOTHETICAL:
                                                                                                     APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
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LOCATION: 153..406
OTHER INFORMATION:
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Pred. No. 5.1e-59;
76; Mismatches 147; Indels
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/327,690
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475.845
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NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IB
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FILING DATE: 24-OCT-1994
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REFERENCE/DOCKET NUMBER: 13952-8-4
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                                                                                                  DRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDK 410
                                EAP 413
                                                                 GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE 432
                                                                                                                                           LVSGWGQLLDRGATA-
                                                                                                                                                                            LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILG 350
                                                                                                                                                                                                              QSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RFS
                                                                                                                                                                                                                                                                                                                         GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                                                                                                                                                             RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA-----SKPQGRIVGGKVCPK 199
                                                                                                                                                                                                                                                                                                                                                                                                SCAPGYKLGDDLLQCHPAVKFPCGRPWKHMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                                                                                                                                                   LDIDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET 295
                                                                                                                                                                                                                                                                                        GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower
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TYPE: amino acid
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33.7%; Score ,..., 5.6e-59;
Local Similarity 38.8%; Pred. No. 5.6e-59;
Conservative 76; Mismatches 147; Indels 36;
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REFERENCE/DOCKET NUMBER: 13
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CLASSIFICATION: 435
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200 GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE 258
                                                                         151 RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA----
                                                                                                            119 SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
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Hart, Charles E.
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US-08-660-289-2
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Patent No. 5833982
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INFORMATION FOR SEQ ID NO: 2:
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APPLICANT:
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APPLICATION NUMBER:
FILING DATE: 21-MAY-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
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NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                             LENGTH:
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Best Local Similarity 38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                  REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
                                                                                                                                                                                                                                    FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Modified Factor VII NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 PRP 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 DRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDK 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 LYTGWGYHSSREKEAKRNRTFYLNFIKIPYVPHNECSEVM-----SNMVSENMLCAGILG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 QSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPBRTFSERTLAFV-RFS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 LDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA---
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amino acid
                      444 amino acids
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Pred. No. 5.6e-59;
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RESULT 49
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Patent No. 5997864
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                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: PATENTIN Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                      FILING DATE:
                                                                                 APPLICATION NUMBER:
                                                                                                                                                     PILING DATE:
                                                                                                                                                                              APPLICATION NUMBER:
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Similarity 38.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                 USA
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Hedner, Ulla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZymoGenetics, Inc
                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08464233 Patent No. 6039944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                    APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                         ZIP: 94105-1492
                                                                                                                                                                                             STATE:
                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                    COUNTRY:
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; Sequence 2, Application US/09189607; Patent No. 6168789
; GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.;
APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
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NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
07/662,920
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CLASSIFICATION:
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FILING DATE: 24-OCT-1994
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APPLICANT:
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TOPOLOGY:
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; MOLECULE TYPE: protein US-09-189-607-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
FILING DATE: 21-MAY-19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
07/662,920
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Modified I
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,990 REFERENCE/DOCKET NUMBER: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/6 FILING DATE: 28-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.24
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259 QSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RFS
                                       236 LDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET 295
                                                                                            200 GECPWQVLLLVNGAQL-CGGTLINTIWVVSÄÄHCFDKIKNWRNLIAVLGEHDLSEHDGDE 258
                                                                                                                                                                                               151 RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA-----SKPQGRIVGGKVCPK 199
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                                                                                                                                                                                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
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RESULT 52
US-09-378-907-2
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                     Query Match 33.7%; Score 783; DB 3; Length 444; Best Local Similarity 38.8%; Pred. No. 5.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hedner, ULIA
APPLICANT: Rasmussen, Mirella E.
AITLE OF TRANSPIROR: Modified Fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hart, Charles E. APPLICANT: Petersen, Lars C. APPLICANT: Hedner, Ulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/378,907
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179 GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                 151
                                                                                          119 SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
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                                                                                                                                                                                                                                                                                  1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                 RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA-----SKPQGRIVGGKVCPK 199
                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
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                                                                                                                                           SPCONGGSCKDOLOSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC 150
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PCT-US94-05779-2
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/0
FILING DATE: 28-FE8-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
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CURRENT APPLICATION DATA:
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                             151
                                                               119 SCAPGYKLGDDLLQCHPAVKEPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
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                                                                                                                                                                                                                                                          1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                        RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA-----SKPQGRIVGGKVCPK 199
                                                                                                                                                               SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                                                                                                                   ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC-----AS 90
                                                                                                                   SPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC 150
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US-07-882-202A-4
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Patent No. 5374617
                                                                                                                                                          Matches 164;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with PV
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERRICE/DOCKET NUMBER: OM
TELECOMMINICATION INFORMATION:
TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
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                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1:
CLASSIFICATION:
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                                                                                                                                                                            Local Similarity
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  113 SPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC 172
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                                                                                                                   1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                             ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC-----AS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDSPMQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
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                                                                                                                                                                                                                                                                                                                466 amino acids
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-1992
                                                                                                                                                  33.7%; Score 783; DB 1; Length 466; 38.8%; Pred. No. 6e-59; tive 76; Mismatches 147; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/07/882,202A
                                                                                                                                                                                                                                                                                                                                                                                                                                  OMRF B34290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/08021615A ; Patent No. 5504064
                                                                          US-08-021-615A-4
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILLING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
                                                                                                                                                                                                                    TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of
TITLE OF INVENTION: Tissue Fact
TITLE OF INVENTION: FVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,966 REFERENCE/DOCKET NUMBER: OM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 75270-2197
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                                                                                                                                                                                                                                                                   TELEPHONE: 214-939-4500
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                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA-----SKPQGRIVGGKVCPK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 PRP 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 QSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RFS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 LDLDIKEVEVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dallas
: Texas
                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Richards, Medlock & Andrews
1201 Elm Street, Suite 4500
                                                                                                                                                                 466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of Bleeding with Modified Tissue Factor in Combination with an Activator of FVII
33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            US 07/882,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/021,615A
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Score 783; DB 1;
Pred. No. 6e-59;
                       Length 466;
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Matches

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RESULT 56
US-08-321-777-4
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                 TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
                                                                                        REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Treatment of Bleeding with Modified TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Morrissey, James H. APPLICANT: Comp, Philip C.
                                                                                                                                                                                      FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Dallas
                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                               NAME: Hansen, Eugenia S.
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SICCGHGTCIDGIGSESCDCRSGWEGRECQ-REVSEINCSIDNGGCTHYCLEEVGWRR-C 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75270-2197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC-----AS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVSGWGQLLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSD 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457
                                                                      214-939-4500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09009217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6132729
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: King, Steven
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMB
TITLE OF INVENTION: CHEM
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 33.7%; Score 783; DB 1; Length 466; Local Similarity 38.8%; Pred. No. 6e-59;
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                                             CLASSIFICATION:
                                                                      APPLICATION NUMBER: FILING DATE: Concur.
                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 77210
                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                        CITY:
                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                        Houston
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                                                                                                                                                                                                                                                                                                            Texas
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P.O. Box 4433
                                                                                                                                                                                                                                                                                        USA
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King, Steven W.
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                                                                      Concurrently Herewith
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  US 60/042,427
                                                                                             US/09/009,217
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                                                                                                                                             Version #1.30
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RESULT 58
US-09-009-656-14
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                                                                                                                                                                                                      Sequence 14, Application US/09009656 Patent No. 6132730 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 14:
                                        APPLICANT: King, Steven
APPLICANT: Gao, Boning
TITLE GAO, BONING
TITLE OF INVENTION: COME
TITLE OF INVENTION: METH
TITLE OF INVENTION: TREE
NUMBER OF SEQUENCES: 27
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REFERENCE/DOCKET NUMBER: UTSD:536
TELECOMMUNICATION INFORMATION:
                                                                                                                                                         APPLICANT:
APPLICANT:
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LENGTH: 466 amino acids
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ATTORNEY/AGENT INFORMATION:
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                       CORRESPONDENCE ADDRESS:
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TELEFAX: 512/474-7577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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ADDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC-----AS 112
                                                                                                                                                         Thorpe, Philip E.
King, Steven W.
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                                               TREATMENT
27
                                                                                      COMBINED TISSUE FACTOR AND FACTOR VIIA METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.7%; Score 783; DB 3; Length 466; 38.8%; Pred. No. 6e-59;
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INFORMATION FOR SEQ ID NO: 14:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 61
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 27-JAN-1997 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 60/042,427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hibler, David W.
REGISTRATION NUMBER: 41
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/036,205
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  4S5 PRP 457
                                             411 EAP 413
                                                                                      395 GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE
                                                                                                                                 351 DRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDK 410
                                                                                                                                                                              340 LVSGWGQLLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSD 394
                                                                                                                                                                                                                         296 LYTGWGYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                                                                                                                                                                                                                                                                  GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE
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76;

Mismatches

36;

Gaps

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280 235 221

DB 3; Length 466; 147; Indels

UTSD:537

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RESULT 59
PCT-US93-04493-4
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APPLICANT: Mortissey, James H.
APPLICANT: Comp, Philip C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 13-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Y.
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: OMRF B34290CIPC/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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296 LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILG 350
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                                            QSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RFS 339
                                                                                 LDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET 295
                                                                                                                                                                         GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                     RCHEGYSLLADGVSCTPTVEYPCGK-IPILEKRNA-----SKPQGRIVGGKVCPK 221
                                                                                                                                 GECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 07-JUN-1995
              NAME/KEY: Modified-site
LOCATION: 46
OTHER INFORMATION: /note= "Location of Intron
FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
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                                                                                                                                                                                                                                                                                                                          FEATURE:
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TELEFAX: 90-4030
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                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                     NAME/KEY: Modified-site
LOCATION: (37^38)
OTHER INFORMATION: /note= "Location
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein LOCATION: 1..139 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Adler, Reid G. REGISTRATION NUMBER: 30,988
                                                                                                                                                                                              OTHER INFORMATION: /note=
                                                                                                                                                                                                               NAME/KEY: Modified-site LOCATION: -17
                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
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LOCATION:
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Modified-site
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US-08-487-037-1
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Best Local Similarity
        GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISO:
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OTHER INFORMATION: /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTTVPICLPDSGLAERELNQAGQET-LVTG 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 P 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 -- CQNQGKCKXGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 151
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2000 Pennsylvania Avenue,
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group(17..2, 50..61, 55..70, 72..81, 89..100, ...
109, 111..124, 132..251, 150..155, 170..186, 299..313, 324..352)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "An amino acid represented
by the greek letter Beta"
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
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LOCATION: /not
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
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TELEFAX: 90-4030
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STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                       NAME/KEY: Peptide LOCATION: -40..0 OTHER INFORMATION:
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OTHER INFORMATION: /note= "Location of Intron A"
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NAME/KEY: Peptide
LOCATION: 143.194
OTHER INFORMATION:
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                                                                    LOCATION: 1..139
OTHER INFORMATION:
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the greek letter Beta"
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     /note= "Activation Peptide"
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                                                                    /note= "Factor Xa- Light chain"
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Patent No. 5621039
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                                                                        OPERATING SYSTEM: DOS 6.0 SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA:
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             PRIOR APPLICATION DATA:
                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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LOCATION:
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CITY: H
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                            APPLICATION NUMBER: FILING DATE: June & CLASSIFICATION: 52
                                                                                                                                                                                          COUNTRY:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 TPITFRMNVAPACIPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 WVLTAAHCMDESKKLLVRIGEYDLRRWEKWELDLDIKEVFVHPNYSKSTIDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 -- CQNQGKCKXGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                         Hauppauge
: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPATLSQTIVPICLEDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED------QVD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEG 442
                                                                                                                                                                                                                                           300 Rabro Drive
                                                                                                                                                                                            USA
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                                                                                                                          E: Diskette, 3
IBM Compatible
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                                                                                                                                                                                                                                                            GALGANO & BURKE
                                            June 8, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 746; DB 1; 33.5%; Pred. No. 9.2e-56;
                                                                                                                                                                                                                                                                                                          Factor IX - Polymeric Conjugates
                                                                                                                                                                                                                                                                                                                         et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Factor Xa-Heavy Chain"
                                                           US/08/073,531B
                                                                                                                                            3.50
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                                                                                                                                            inch,
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                                                                                                                                            1.44
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                                                                                                                                           Mb Storage
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RESULT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
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; RELEVANT RESIDUES IN SEQ ID NO: US-08-073-531B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 582-6191
INFORMATION FOR SEQ ID NO: 1:
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CELL TYPE:
IMMEDIATE SOURCE:
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE: ORGANISM: -
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LENGTH: 415 Amino Acid
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REGISTRATION NUMBER: 30,735
REFERENCE/DOCKET NUMBER: 128-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 582-6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: -
ATTORNEY/AGENT INFORMATION:
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404 YVNWI 408
                                                         399 YLDWI 403
                                                                                                                       344 IYNNMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSR 403
                                                                                                                                                                             339 VSENMICAGIIGDRQDACEGDSGGPMVASFHGTWFIVGIVSWGEGCGLLHNYGVYTKVSR 398
                                                                                                                                                                                                                                                 293 KEYTNIFLKFG--SGYVSGWGRVFHKGRS--
                                                                                                                                                                                                                                                                                                                                                                     233 AGEHNIEETEHTEOKKNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIAD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                  223 LGEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 SFNDFTRVVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 -----RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 YRLAENQKSCEPAVPFPCGRVSVSQTSKLTRAEAVFPD-VDYVNPTEAETILDNITQGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 YKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 NGGSCKDDINSYECWCPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LEELRHSSLERECIEBICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC
                                                                                                                                                                                                                                                                                                       SGLAERELNQAGQETLVTGWG--YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNM 338
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                                                                                                                                                                                 Matches
                                                                                                                                                                                                                Query Match
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APPLICANT: Hallaha
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INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 415 Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,531
FILING DATE: June 8, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Worderfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,735
REFERENCE/DOCKET NUMBER: 128-7 (DIV)
REFERENCE/TOCKET NUMBER: 128-7 (DIV)
REFERENCE/TOCKET NUMBER: 30,735
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                                                                                                                                                                                                Local Similarity
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CELL TYPE: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: - CLASSIFICATION:
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OPERATING SYSTEM:
SOFTWARE: Wordper
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STATE: New York
                                                                                                                                                                                                                                                                                                                                            VOLUME:
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                                                                                                                                                                                                                                                                                                         PAGES:
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124 YKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDP-
                                58 NGGSCKDDINSYECWCPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG 114
                                                                65 GHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
                                                                                                                                      5 LEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCASLCC 64
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                                                                                                      LEEFVEGNLERECMEEKCSFEEAREVFENTEKTTEFWKQYVDGDQCESNP-
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                                                                                                                                                                              Conservative
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Factor IX -
                                                                                                                                                                            31.9%; Score 742; DB 2; I
35.8%; Pred. No. 1.7e-55;
tive 69; Mismatches 156;
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                                                                                                                                                                                                                                                                                          TELEX: 90-4030
INPORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 2803
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 887-0763
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PAtentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
FEATURE: Peptide
                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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                                                                                          FEATURE:
                                                      NAME/KEY:
LOCATION:
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                                      OTHER INFORMATION:
                                                                                                          OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                             NAME/KEY: Modified-site LOCATION: -40..397
                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 KEYTNIFLKFG--SGYVSGWGRVFHKGRS-----ALVLEYLRVPLVDRATCLRSTKFT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 LGEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 SENDETRVVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVV 232
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DC
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                                                                                                                                                                                                                                                       437 amino acids
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                                      /note= "Factor Xa - Light Chain"
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                                                                                                            "Same features apply from NO:2"
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US-08-487-037-3
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NAME/KEY:
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                          P 419
                                                      AGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHA
                                                                               SGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWA 418
                                                                                                                                                                 EVVIKHNRFTKETYDFNIAVLRLKTPITFRMNVAPACLPERDWAESTL--MTQKTGIVSG
                                                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET-LVTG
                                                                                                                                                                                                                                                                              ARGYTLADNGKACIPTGPYPCGK--QTLERRKR-----
                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                           FGRTHEKGRQSTR-----LKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGD
                                                                                                                                     WGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGD
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by the greek letter Beta"
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Pred. No. 2e-
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US-08-742-877-2
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COUNTRY:
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APPLICANT: MEULIEN, PIERRE
TITLE OF INVENTION: DNA SEQUENCE CODING POR HUMAN FACTOR;
IX OR A SIMILAR PROTEIN, EXPRESSION VECTOR, TRANSFORMED CELLS,
METHOD FOR PREPARING FACTOR IX AND CORRESPONDING PRODUCTS OBTAINED;
                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08742877 Patent No. 6046380
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FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 970,966
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 433,276
                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: CLARK,
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CURRENT APPLICATION DATA:
                                             NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                          TITLE OF INVENTION:
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STREET: 1100 ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PRLIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKK 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                         CLARK, Anthony J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 736.5; DB 6; Length 461; 35.7%; Pred. No. 5.6e-55; tive 72; Mismatches 157; Indels 47;
                                                                                                                                                                                          DNA SEQUENCES
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                                                                                                                                 RESULT 67
US-09-053-871A-21
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REFERENCE/DOCKET NUMBER: 0623
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
IELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                      Sequence 21, Application US/09053871A
Patent No. 6315995
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                                                                   GENERAL INFORMATION:
                     APPLICANT:
APPLICANT:
  APPLICANT:
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FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/742,877
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: FLESHNER, RAZ E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 YKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKR-----DTEDQEDQVD------
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                                                                                                                                                                                                                               451 VNWI 454
                                                                                                                                                                                                                                                                               400 LDWI 403
                                                                                                                                                                                                                                                                                                                           391 YNNMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRY 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 GEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPDS 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLAERELNQAGQETLVTGWG--YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNDFTRVVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEEFVQGNLERECMEEKCSFEEAREVFENTBRTTEFWKQYVDGDQCESNP------
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                                                                                                                                                                                                                                                                                                                                                                    SENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRY 399
Pinsky, David
Stern, David
Rose, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/10133907 ; Patent No. 6677369
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; SEQ ID NO 21
; LENGTH: 461
US-10-133-907-5
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APPLICANT: Schmidt, Ann M
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: STROK
FILE REFERENCE: 51917-B
                                                                                        PRIOR APPLICATION NUMBER: 60/286,314
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 5
SOFTMARE: PatentIn version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor V. TITLE OF INVENTION: with vesicle vector FILE REFERENCE: 6627-FA1170
                                                                                                                                                                                                                                                                                                                        APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/133,907 CURRENT FILING DATE: 2002-04-25
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ORGANISM: Homo Sapien
                       ORGANISM: Homo sapiens
                                               TYPE: PRT
                                                                LENGTH: 461
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35.4%; Pred. No. 6.2e-55;
rative 72; Mismatches 156;
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                                                                                                                                                                                                          Query Match 31.6%; Score 735; DB 4; Length 415; Best Local Similarity 35.4%; Pred. No. 6.6e-55; Matches 150; Conservative 72; Mismatches 156; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09118748A Patent No. 6531298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/118,748A CURRENT FILING DATE: 1998-07-17 EARLIER APPLICATION NUMBER: 60/053,571 EARLIER FILING DATE: 1997-07-21 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Factor Ix Antihemophilic Factor with Increased Clotting TITLE OF INVENTION: Activity FILE REFERENCE: 5470-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stafford, Da APPLICANT: Chang, JinLi
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 31.7%; Score 736; DB 4; Length 461; Local Similarity 35.4%; Pred. No. 6.2e-55; hes 150; Conservative 72; Mismatches 156; Indels 46;
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124 YKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKR-----DTEDQEDQVD------ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
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                                      58 NGGSCKDDINSYECWCPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG 114
                                                                                 65 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
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                                                                                                                          6 LEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVDGDQCESNP-----CL 57
                                                                                                                                                                   5 LEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC 64
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US-08-295-411-2
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                                                                                                                                                                   TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC
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TITLE OF INVENTION:
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MEDIUM TYPE: Floppy
                                                           MOLECULE TYPE:
HYPOTHETICAL: I
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                                        ANTI-SENSE:
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CITY: La Jolla
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SOFTWARE: PatentI
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                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
NAME/KEY: Region
                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405
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Mesters, Rolf M.
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SYSTEM: PC-DOS/MS-DOS
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                                                        NO Protein
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APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serime PA
TITLE OF INVENTION: Anti-Pept
TITLE OF INVENTION: for Inhil
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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150;
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 146..180 OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..145
OTHER INFORMATION:
                                                                                                             CITY: La Jolla
STATE: CA
                                                                         ZIP: 92037
                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 LGEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPD 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLAERELNQAGQETLVTGWG--YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG
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181..415
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; Pred. No. 1.5e-54; 
69; Mismatches 158; Indels
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US-08-955-471-2
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INFORMATION FOR SEQ ID NO: 2:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
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LOCATION: 181..415
OTHER INFORMATION:
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399 YLDWI 403
                                                344 IYNNMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSR 403
                                                                                                                                                                                                                                         233 AGEHNIEETEHTEOKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIAD
                                                                                                                                                                                                                                                                              223 LGEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPD 280
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                                                                                           339 VSENMLCAGILGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSR 398
                                                                                                                                           293 KEYTNIFLKFG--SGYVSGWARVFHKGRS-----ALVLQYLRVPLVDRATCLRSTKFT 343
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                                                                                                                                                                                        SGLAERELNQAGQETLYTGWG--YHSSREKEAKRNRTFYLNFIKIPYVPHNECSEVMSNM 338
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                                                                                                                    Matches
                                                                                                                                                 Query Match
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MOLECULE TYPE: pro
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TITLE OF INVENTION: Ant
TITLE OF INVENTION: for
NUMBER OF SECTEDUS: 10
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/793,989 FILING DATE: 18-NOV-1991 ATTORNEY/AGENT INFORMATION:
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LENGTH: 415 amino acids
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LOCATION: 146..180
CTHER INFORMATION: /
OTHER INFORMATION: F
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                                                                                                                                                                                                NAME/KEY: Region
LOCATION: 181..419
OTHER INFORMATION:
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC
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STATE:
                                                                                                                               Match 31.5%; Score 731; DB 5; Local Similarity 35.3%; Pred. No. 1.5e-54;
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                 65 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWR-RCSCAPG 123
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181..415
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Rolf
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                                         APPLICATION NUMBER: US 07
APPLICATION NUMBER: US 07
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAMB: Agris, Cheryl H.
                                                                                                                                                                             FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-NOV-1989
                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSES: No. 55805
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                                                                                                                                                               PRIOR APPLICATION DATA:
 TELECOMMUNICATION INFORMATION:
                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                               APPLICATION NUMBER: FILING DATE: 24-JUN
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                               24-JUN-1988
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                                                                                              US 07/898,248
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344 IYNNMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSR 403
                                                                                             339 VSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSR 398
                                                                                                                                                                                                                                                                                               281 SGLAERELNQAGQETLYTGWG--YHSSREKEAKRNRTFYLNFIKIPYYPHNECSEVMSNM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 SENDETRVVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 YRLAENQKSCEPAVPFPCGRVSVSQTSKLTRAEAVFPD-VDYVNPTEAETILDNITQGTQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 LGEYDLRRWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 YKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDP----- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 NGGSCKDDINSYECWCPFGFEGKNCELDVT---CNIKNGRCEQFCKNSADNKVVCSCTEG 114
                                                                                                                                                                                           KEYINIFLKFG--SGYVSGWARVFHKGRS-----ALVLQYLRVPLVDRATCLRSTKFT 343
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APPLICANT: Bjorn, Soren B.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SEQUENCES: 26 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US 405 Lexington Avenue, 62nd Floor No. 55805600 No. 5580560disk of No. 5580560th America, Inc US 07/434,149 PCT/DK88/00103

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                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6086871
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08952967
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
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      COUNTRY: USA
ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                          TITLE OF INVENTION: PROTHROMBIN DERIVATIVES NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       APPLICANT: Mitterer, Artur
APPLICANT: Falkner, Falko-Guenter
APPLICANT: Eibl, Johann
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fischer, Bernhard APPLICANT: Schlokat, Uwe
CURRENT APPLICATION DATA:
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                                                                                                                                                                  STATE:
                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPCQNGGSCKPQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANAFLYYLRPGSLYRYCKYYQCSFYYARYIFKDAYRTKLFWISYSDGDQC-----AS 52
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                                                                                                                                                                  D.C
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A
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                                                                                                                                                                                                                               393 ASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPR 452
572 FVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWI 613
                                                                                                                  307
                                                                                                                                                                                            249
                                                                                                                                                                                                                                                                      198 AVLIHPSWYLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPN 248
                                                                                                                                                                                                                                                                                                             335 DCGLRP--LFEKKSLEDKTERELLESYIDGRIVEGSDAEIGMSPWQVMLFRKSPQELLCG
                                                                                                                                                                                                                                                                                                                                                                                           275 YVAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 QQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW----C 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 G---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 NPDSSTMGPWCYTTDPTVRRQECSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 ---CLEGNCAEGLGTNYRGHVNITRSGIECQP-WRSRYPHKPEINSTTHPGADLQENFCR 158
                                      364 MV--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                       453
                                                                                                                                                                                                                                                                                                                                                  140 PCG-RPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLL-DSKKKLACG 197
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                                                                           TANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGP
                                                                                                                EKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGP 363
                                                                                                                                                                                          YS-KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWG-YHSSR 306
                                                                                                                                                       YNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETA-ASLLQAGYKGRVTGWGNLKETW 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -YCL----
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RESULT 75 US-08-295-411-4 ; Sequence 4, Application US/08295411

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Griffin,
APPLICANT: Mestcars,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793, 989
FILING DATE: 18-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TS TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U:
ZIP: 92037
                                                                                                                                                                                                                                                                                                                    / Match 24.2%; Score 562.5; DB 1; Length 579;
Local Similarity 28.9%; Pred. No. 5.6e-40;
1es 168; Conservative 63; Mismatches 160; Indels 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Region
LOCATION: 1..320
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region LOCATION: 321..579 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 22-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
176 QQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEBGVW----C 231
                                          104 G-----CTH----
                                                                            116 NPDSSNTGPWCYTTDPTVRRQECSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRG 175
                                                                                                                        91
                                                                                                                                                          60 ---CLEGNCAEGLGINYRGHVNITRSGIECQL-WRSRYPHKPEINSTTHPGADLQENFCR 115
                                                                                                                                                                                                  61 SLCCGHGTCIDGIGS-----FSCDCRSGWEGR----
                                                                                                                                                                                                                                                                  1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                          1 ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATDVFWAKYTACETART-PRDKLAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i: 579 amino acids amino acid
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Rolf M.
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Prothrombin Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Prothrombin Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/295,411
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                                      ----YCL----EEVGWRRCSC 120
                                                                                                                    --EVSFLN-----CSLDNG 103
                                                                                                                                                                                                                                                                                                                         Indels 191;
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                                                                                                                                                                                                  FCQ 90
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                                                                                                                                     TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,16
REFERENCE/DOCKET NUMBER: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
                                                                                                                  SEQUENCE CHARACTERISTICS:
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  ANTI-SENSE:
                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
COUNTRY: USA
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                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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                                                                                                                                                                             TELEPHONE:
                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 PCG-RPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLL-DSKKKKLACG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 YVAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEA 291
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                                                                                        579 amino acids
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                                                         linear
            . protein
                                                                                                                                                                               619-554-2937
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US-09-117-708-14
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                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09117708
Patent No. 6060300
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                          APPLICANT: HOEFFKEN,
APPLICANT: and RUBSA,
TITLE OF INVENTION: T
TITLE OF INVENTION: UNUMBER OF SEQUENCES:
STREET: LIVE
CITY: Washington
STATE: D.C.
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                                                                                                           CORRESPONDENCE ADDRESS:
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LOCATION:
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OTHER INFORMATION:
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                                                                   ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 PCG-RPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLL-DSKKKLACG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 YVAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 APGYKLGD----DLLQCHPAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 G--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 NPDSSNTGPWCYTTDPTVRRQECSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 MV--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SLCCGHGTCIDGIGS-----FSCDCRSGWEGR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YS-KSTTUNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWG-YHSSR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANVGKGQPSVLQVVNLPIVERPVCKDSTRITIDNMFCAGYKPDEGKRGDACEGDSGGP 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETA-ASLLQAGYKGRVTGWGNLKETW 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYBRNIEKISMLEKIYIHPR 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVLIHPSWVLTAAHCM----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQYQGRLAVITHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW-----C
                                                                                                                                                                                                                                                                                                                                                                                                                   FVMKSPENNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWI 570
                                                                                                                                                                                       BOLLSCHWEILER, Claus; SCHMIDT, Martin; HOEFFKEN, Hans Wolfgang; SCHWEDEN, Juergen; and RUEBSAMEN, Klaus
                                                                                                                                                                                                                                                       RADITSHC, Martin; FRIEDRICH, Thomas;
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                                                                                                                                                   thrombin inhibitors
                                                                                                                                                                      Thrombin muteins as antidote for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Prothrombin Heavy Chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Prothrombin Light Chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 562.5; DB 2
Pred. No. 5.6e-40;
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RESULT 78
PCT-US92-10242-4
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Sequence 4, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serine Proteas
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
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LENGTH: 579 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM AT-compatible, Pentium OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect version 6.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 QYQGRLAVITHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW----CY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                  411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 VAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEQQTFFNPRTFGSGEAD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 -----CTH-----
                                                                                                                                                                                              530 VMKSPĖNNRWYQMGIVSWGĖGCDRDGKYGFYTHVFRLKKWI 570
                                                                                                                                                                                                                                                                                                                                                                                                        250 S-KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWG-YHSSRE 307
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                                                                                                                                                                                                                                                                                ANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMPCAGYKPDEGKRGDACEGDSGGPF
                                                                                                                                                                                                                                                                                                                      KEAKRNRIFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGPM 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRY 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGYKLGD----DLLQCHPAV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CLEGNCAEGLGTNYRGHVNITRSGIECQLWRSRYPHKPEINSTTHPGADLQENFCRN 116
                                                                                                                                                                                                                                      V--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                  NWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETA-ASILQAGYKGRVTGWGNLKETWT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLIHPSWVLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPNY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGLRP--LFEKKSLEDKTERELLESYIDGRIVEGSDAEIGMSPWQVMLFRKSPQELLCGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.2%; Score 562.5; DB 3; ilarity 29.1%; Pred. No. 5.6e-40; Conservative 62; Mismatches 161;
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Serine Protease-Derived Polypeptides and

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; LOCATION: 321..579
; OTHER INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
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TENGTH: 5/7 ....
TYPE: AMINO ACID
Tinear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                    176
                                                                                                                                   104
140 PCG-RPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLL-DSKKKLACG 197
                               232 YVAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEA 291
                                                                 121 APGYKLGD----DLLQCHPAV-
                                                                                                                                                                    116 NPDSSNTGPWCYTTDPTVRRQECSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRG 175
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                                                                                                  QQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW----C 231
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321..579
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                                                                                                                                                                                                                                                                                                                                                                                                  24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-Peptide Antibodies, Systems and Therapeutic Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Prothrombin Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Prothrombin Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US92/10242
                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 562.5; DB 5; Length 579; Pred. No. 5.6e-40;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 160;
                                                                                                                                     ----YCL----EEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                 Indels 191;
                                                                                                                                                                                                         -EVSFLN-----CSLDNG 103
                                                                 -----KF 139
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                             -FCQ 90
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                                                                Local
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RESULT 79
US-07-998-972A-3
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                                                                         Matches 168;
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPILICANT: Holly, Richard D.
APPILICANT: Foster, Donald C.
TITLE OF INVENTIONS: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                  LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 DCGLRP--LFEKKSLEDKTERELLESYIDGRIVEGSDAEIGMSPWQVMLFRKSPQELLCG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 MV--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 TANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGP 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 EKBAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 YNWRENLDRDIALMKLKKPVAFSDYÍHÞVCLÞDRETÁ-ASLLQÁGYKGRVTGWGNLKETW 468
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1 ANSFLEELRHSSLERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94105
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                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYBRNIEKISMLEKIYIHPR 409
                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                  615 amino acids
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19921230
                                                                                                  24.2%; Score 562.5; DB 1; 28.9%; Pred. No. 6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/816,281
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                                                                            63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        13952-12-2
                                                                              160;
                                                                                 Indels 191;
                                                                                                                         Length 615;
                                                                                 Gaps
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RESULT 80
US-08-463-953-3
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3,
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 31-DEC-1991
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION: NAME: Parmelee, Steven W
                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
                                                                                                                                                                   CLASSIFICATION: 514
                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATDVFWAKYTACETART-PRDKLAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVLIHPSWVLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW---
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                                                                                                                       US 07/860,701
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                                                             US 07/816,281
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                                                                                                                                                                                                                                                                           RESULT 81
US-08-462-261-3
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                                                                                                                                                                                                        Sequence 3, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
  NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSES: Trownsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twencieth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                             APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
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Š 뮍 Ś Вþ Ş 밁 Ş B ΩV 문 Ś 밁 5 뮍 Ş В Ş 밁

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US-08-463-953-3
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REFERENCE/DOCKET NUMBER: 1395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                  446
                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                        386 ASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPR 445
                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                 328 DCGLRP--LFEKKSLEDKTERELLESYIDGRIVEGSDAEIGMSPWQVMLFRKSPQELLCG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 PCG-RPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLL-DSKKKKLACG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 YVAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 APGYKLGD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 G-----CTH-----
                                                   364 MV--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGS-----FSCDCRSGWEGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATOVFWAKYTACETART-PROKLAA 95
                                                                                                                                                                                                                                                                                                                                                                        AVLIHPSWVLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW----C 267
                                                                                                                                                            EKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGP 363
FVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWI 606
                                                                                                      TANVGKGQPSVLQVVNLÞIVERÞVCKDSTRIRITDNMFCAGYKÞDEGKRGDÁCEGDSGGÞ 564
                                                                                                                                                                                                               YNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETA-ASLLQAGYKGRVIGWGNLKETW 504
                                                                                                                                                                                                                                                                     YS-KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWG-YHSSR 306
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28.9%; Pred. No. 6e-40;
1tive 63; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DLLQCHPAV-
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Best Local :
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEGISTKATION NUMBER: 31,990
REFERENCE DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-MAR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/462,261
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                                                                                  446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
505 TANVGKGQPSVLQVVNLPIVERPVCKDSTRITIDNMFCAGYKPDEGKRGDACEGDSGGP 564
                                      307 EKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGGP 363
                                                                                                                           249 YS-KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLYTGWG-YHSSR 306
                                                                                                                                                                      386 ASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPR 445
                                                                                                                                                                                                               198 AVLIHPSWVLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPN 248
                                                                                                                                                                                                                                                          328 DCGLRP--LFEKKSLEDKTERELLESYIDGRIVEGSDAEIGMSPWQVMLFRKSPQELLCG 385
                                                                                                                                                                                                                                                                                                                                              268 YVAGKPGDFGYCDLNYCEEAVEEETGDGLDEDSDRAIEGRTATSEYQTFFNPRTFGSGEA 327
                                                                                                                                                                                                                                                                                                                                                                                          121 APGYKLGD----DLLQCHPAV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 24.2%; Score 562.5; DB 1; Length 615; Similarity 28.9%; Pred. No. 6e-40;
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                                                                                  YNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETA-ASLLQAGYKGRVTGWGNLKETW 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G----CTH-----
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SYSTEM: PC-DOS/MS-DOS
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PCT-US92-11357-3
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Townsend and Townsend STREET: One Market Plaza, Stewar
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APPLICANT: FOSter, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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FILING DATE: 31-MAR-1992
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CLASSIFICATION:
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212 QQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVW---
                                                                           152 NPDSSNTGPWCYTTDPTVRRQECSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRG 211
                                                                                                                                                         96 --- CLEGNCAEGLGTNYRGHVNITRSGIECQL-WRSRYPHKPEINSTTHPGADLQENFCR 151
                                                                                                                                                                                                                                          37 ANTFLEEVRKGNIERECVEETCSYEEAFEALESSTATDVFWAKYTACETART-PROKLAA 95
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                                                                                                                                                                                                    61 SLCCGHGTCIDGIGS-----
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                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 615;
                                                                                                                      --EVSFLN-----CSLDNG 103
                                        --YCL----EEVGWRRCSC 120
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121 APGYKLGD----DLLQCHPAV--

-KF 139 -C 267 -FCQ 90

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                                                                               US-08-338-368-2
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GENERAL INFORMATION:
APPLICANT: GIBBS,
Best Local Similarity Matches 112; Conserv
                                     Query Match
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TSIANG,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                              TOPOLOGY: li
                                                                                                                                                                                                                                     NAME: HENSLEY, MAX D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-574-3000
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GILEAD SCIENCES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 353 LAKESIDE DRIVE CITY: POSTER CITY
                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 FVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWI 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALIFORNIA
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                                                                                                                                                           295 amino acids
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Conservative
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                                                                                                                     linear
                                                                                                protein
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                  20.5%; Score 475.5; DB 3; 39.9%; Pred. No. 6.8e-33;
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  43; Mismatches 105;
                                                                                                                                                                                                                                                                                   190.2
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                                     Length 295;
  Indels
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Gaps
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US-09-027-337-7
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CURRENT PILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 7
LENGTH: 255
TYPE: PRT
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APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed
TITLE OF INVENTION: Breast and Ovarian Carcinomas
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Patent No. 5972616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 VLIHPSWVLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHPNY 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 V--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                 169 RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 SLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRY 126
                                                                                                                            341 ENMICAGIIGDRQDACEGDSGGEMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYL 400
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234 EWLQKLMRSEPRP 246
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                                                                                                                                                                                                                                                                  60 HDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIÄLLRLHQPVVLTDHVVPLCLPERTFSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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                                       DWIHGHIRDKEAP 413
                                                                                                                                                                           RTLAFV-RFSLVSGWGQLLDRGATA-
                                                                                                                                                                                                                      RELNQAGQETLVTGWGYHSSREKBAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVS 340
                                                                                                                                                                                                                                                                                                                 YDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAE 285
                                                                                       EYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                20.4%; Score 473.5; DB 2; 37.9%; Pred. No. 8.4e-33; tive 52; Mismatches 90;
                                                                                                                                                                              ---LELMVLNVPRLMTODCLQQSRKVGDSPNIT
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; Sequence 7, Application US/09644600; Patent No. 6451500; GENERAL INFORMATION:

US-09-644-600-7

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                                                                                            ; OTHER INFORMATION: Factor 7 US-09-654-600A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
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Patent No. 6649741
Query Match 20.4%; Score 473.5; DB 4; Length 255; Best Local Similarity 37.9%; Pred. No. 8.4e-33; Matches 96; Conservative 52; Mismatches 90; Indels 15
                                                                                                                                                                                                                                    SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION UNMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
NUMBER: 0F SEQ ID NOS: 98
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APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REPERBNCE: D6064CIP/D
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/421,213
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 98
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                                                                                                                                          FEATURE:
                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                      TYPE: PRT
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Local Similarity 37.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIÄLLRLHQPVVLTDHVVPLCLPERTFSE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWLQKLMRSEPRP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELNOAGOETLYTGWGYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVM-----SNMVS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 473.5; DB 4; Length 255; Pred. No. 8.4e-33;
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                                                                                     ; ORGANISM:
US-08-148-910-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08148910 Patent No. 5466593
Query Match 20.4%; Score 473.5; DB 1; Best Local Similarity 28.3%; Pred. No. 2.7e-32; Matches 141; Conservative 58; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: No. 5466593ember 5, 1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 655 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 5.25 inch, MEDIUM TYPE: 500 Kb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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                                                                                                                                                                 STRANDEDNESS: SII
TOPOLOGY: linear
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                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 EWLOKLMRSEPRP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 RTLAFV-RFSLVSGWGQLLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNIT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 RELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 YDIRRWEKWELDLDIKEVFVHPNYSKSTIDNDIALIHLAQPATISQTIVPICLPDSGLAE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 HDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQEVVLTDHVVELCLEERTESE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RIVGGKVCPKGECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGE 59
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                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
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                                                                                                                                                                                                                               655 amino acids
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                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHIMOMURA et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 5466593el Protein and Gene Encoding Said Protein 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MS-DOS
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                                              Length 655;
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Indels 131;

Gaps

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US-08-448-937A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Takeshi SHIMOMURA et al.
TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 5677164ember 5,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08, FILING DATE: May 24, 1995
                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                              NAME: Warren M. Cheek, Jr
REGISTRATION NUMBER: 33,30
                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 WNSDLLYQELHVDSVGAAALLGLGPHAYCRNPDNDERPWCYVVKDSALSWEYCRLEACES 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTFGIEKYIPYTLYSVFNPSDHDLVLIRLKKKGDRCATRSQFVQPICLPEPG----STFP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPWLAAIYIGDS----FCAGSLVHTCWVVSAAHCFSHSPPRDSVSVVLGQHFFNRTTDVT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPW--QVVILDSKKKLACGAVLIHPSWVLTAAHCMDES---KKLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GGTCHLIVATGTTVCACPPGFAGRLCNIEPD-ERCFLGNGTGYRGVASTSASGLSCLA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGHGTC--IDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDLDIKEVFVHPNYSK-STTDNDIALLHLAQP----ATLSQTIVPICLPDSGLAERELNQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMLCAGYFDCKSDACQGDSGGPLACEKNGVAYLYGIISWGDGCGRLHKPGVYTRVANYVD 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGHKCQIAGWGHLDENVSGYSSSLREA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
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805 Fifteenth
                    202-371-8856
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                                                                                                                                                                                                                                                                                                                                    IBM Compatible
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                                                                                                                                                                                                                                                       US/08/448,937A
                                                                                          33,367
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Street, N.W.,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                     ADDRESSEE: Morrison
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STREET: 2000 STREET: Washington

2000 Pennsylvania Avenue, NW

Morrison & Foerster

STATE: I

USA

ZIP: 20006-1888

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US-08-448-937A-12
               Sequence 1, Application US/08330978
Patent No. 5589571
GENERAL INFORMATION:
APPLICANT: King, Robert
TITLE OF INVENTION: FORMS OF ACT
                                                                                                                                                                       US-08-330-978-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 28.3 Matches 141; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 AGQETLVTGWGY-----HSSREKEAKRNRTFVLNFIKIPVVPHNECS--EVMSNMVSE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 QTFGIEKYIPYTLYSVFNPSDHDLVLIRLKKKGDRCATRSQFVQPICLPEPG----STFP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 HPWLAAIYIGDS----FCAGSLVHTCWVVSAAHCFSHSPPRDSVSVVLGQHFFNRTTDVT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SPW--QVVLLDSKKKLACGAVLIHPSWYLTAAHCMDES---KKLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 LTRVQLSPDLLATLPEPASPGRQACGRRHKKRTFLR-----PRIIGGSSSLPGS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 APGYKLGDDLLQCHEAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 WNSDLLYQELHVDSVGAAALLGLGPHAYCRNPDNDERPWCYVVKDSALSWEYCRLEACES 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 --GGTCHLIVATGTTVCACPPGFAGRLCNIEPD-ERCFLGNGTGYRGVASTSASGLSCLA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 KDCGTEKCFDETRYEYLEGGDRWARVROCHVEQCECFGGRTWCEGTRHTACLSSPCLN-- 252
                                                                                                                                                                                                                                                                               640
                                                                                                                                                                                                                                                                                                                          402 WIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                               342 NMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLD 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 LDLDIKEVFVHPNYSK-STTDNDIALLHLAQP----ATLSQTIVPICLPDSGLAERELNQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CGHGTC--IDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 RECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCL-----VLPLEHPCASLC 63
                                                                                                                                                                                                                                                                                                                                                                               AGHKCQIAGWGHLDENVSGYSSSLREA-----LVPLVADHKCSSPEVYGADISP 579
                                                                                                                                                                                                                                                                             WINDRIR---PPRRLVAP 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    655 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                  PROCESS FOR PRODUCTION OF INHIBITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12:
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                          OF ACTIVATED BLOOD FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCTHYCL----EEVGW--
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                                                                                                           US-08-474-042-1
                                                                                                                             RESULT 90
                                                                     Sequence 1, Application US/08474042
Patent No. 5589572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
GENERAL INFORMATION:
APPLICANT: King, Robert
TITLE OF INVENTION: PRO
TITLE OF INVENTION: FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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NAME: MURASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0007.02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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LOCATION:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "Disulfide linkage to OTHER INFORMATION: residue 132 of SEQ ID NO:2"
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                                                                                                                                                                                                                                                                                                                                 149
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                                                                                                                                                                                                                                                                                                                                                                  266 PATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                             206 VLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQ 265
                                                                                                                                                                                  262 ARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 297
                                                                                                                                                                                                                     385 GLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                          202 YVDRNSCKLSSSFIITONMFCAGYDTKOEDACOGDSGGPHVTRFKDTYFVTGIVSWGEGC 261
                                                                                                                                                                                                                                                                                        325 VVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGC 384
                                                                                                                                                                                                                                                                                                                                                                                                      89 ILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 TENPFOLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEFY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 20.2%; Score 469; DB 1; Similarity 34.8%; Pred. No. 2.6e-32;
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(202)822-0168
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233..261
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PROCESS FOR PRODUCTION OF INHIBITED FORMS OF ACTIVATED BLOOD FACTORS
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US-08-474-042-1
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LOCATION:
FEATURE:
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APPLICATION NUMBER: US 08/484,558
PILING DATE: 07-UNN-1995
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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LOCATION:
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Disulfide-bond LOCATION: 160
OTHER INFORMATION: /note= "Disulfide linkage to OTHER INFORMATION: residue 132 of SEQ ID NO:2"
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STRANDEDNESS: si:
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ZIP: 20006-1888
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                                                                                                                                                                                                                                                                                                                                               Match 20.2%; Score 469; DB 1; Length 306; Local Similarity 34.8%; Pred. No. 2.6e-32;
202 YVDENSCKLSSSEIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGC 261
                                      325 VVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGC 384
                                                                                                                                                                                                 206 VITAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQ 265
                                                                                                                                                                                                                                                                                       159 TEDQEDQVD-----
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                                                                               PITERMAVAPACLPERDWAESTL--MTQXTGIVSGFGRTHEXGRQSTR-----LKMLEVP 201
                                                                                                                        PATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIP 324
                                                                                                                                                                 ILTAAHCLYQAKREKVRVGDRNTEQBEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLKT 148
                                                                                                                                                                                                                                            TENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTTLSEFY 88
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2000 Pennsylvania Avenue, NW
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208..222
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murashige, Kate H. REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                 206 VLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQ 265
                                                                                                                 29 TENPFOLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEFY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20006-1888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONE: (202)887-1500

(: (202)822-0168

90-4030 MRSNFOERSWSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
233..261
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59..64
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                                                                                                                                                                                                                                                                                              20.2%; Score 469; DB 1; Length 306; 34.8%; Pred. No. 2.6e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Disulfide linkage to residue 132 of SEQ ID NO:2"
                                                                                                                                                                                                                                                            60;
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                                                                                                                                                                                     ---PRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSW 205
                                                                                                                                                                                                                                                                Mismatches
:: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - :: - ::
                                                                                                                                                                                                                                                                98; Indels
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RESULT 92
US-08-774-592-1
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APPLICANT: King, 1
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-OCT-1994
CLASSIFICATION: 530
APPLICATION NUMBER: US 08/484
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MUTABÓIGE, Kates H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                   FEATURE
                                     NAME/KEY: Disulfide
LOCATION: 160
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAFIING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-Dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20006-1888
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STREET: 2000 Pennsylvania Avenue,
NAME/KEY:
                                                                                                                                         LOCATION:
                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 YVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 VVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGFMVASFHGTWFLVGLVSWGEGC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 ARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 GLIHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
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                                                                                                                                                                                                                                                                                                     amino acid
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  Disulfide-bond
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                                                                                              Disulfide-bond
                                                                                                                                         Disulfide-bond
79..95
                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROCESS FOR PRODUCTION OF INHIBITED
                                        /note= "Disulfide linkage to residue 132 of SEQ ID NO:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/484,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/774,592
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DB 3;

90; Indels 15; Length 254;

Gaps

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; LOCATION:
US-08-774-592-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50,
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APPLICANT: COHEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Abbott
CITY: Abbott Park
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                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 PITFRMNVAPACLPERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEVP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 TEDQEDQVD------PRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSW 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 ARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 VLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 ILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 TENPFOLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEFY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      b 20.2%;
Similarity 34.8%;
                                                                                                                                                                                                                                                                                                                                                                                             60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08944483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STROUPE, STEVEN D.
VENTION: NOVEL SERINE PROTEASE REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RUSSELL, JOHN C.
STEWART, KENT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
233..261
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                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                          US/08/944,483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08330978
Patent No. 5589571
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
      TELEFAX: (202)822-0168
TELEX: 90-4030 MRSNFOERSWSH
INPORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                              COMPUTER RBADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: King, ROTITLE OF INVENTION:
                                                                                                                                                                         FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,558
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)887-1500
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STRANDEDNESS: single
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TELEX:
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                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 28-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                           REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                   NAME: Murashige, Kat
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TLAFV-RFSLVSGWGQLLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNITE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 ELNQAGQETLYTGWGYHSSREKEAKRNRTFYLNFIKIPVVPHNECSBVM-----SNMVSE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 DIRRWEKWELDLDIKEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAER 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 LIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 DISEHDGDEQSRRVAQVIIPSTYVPGTTNHDIÄLLRIHQPVVLTDHVVPLCLPERTFSER 119
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                                                                                                                                                                                                                                                                                       28-OCT-1994
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37.7%;
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Pred. No. 2.2e-32;
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US-08-474-042-3
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Patent No. 5589572
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                       APPLICANT: King, Robert TITLE OF INVENTION: PROCESS E TITLE OF INVENTION: FORMS OF
                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                ADDRESSEE: Morrison & Foerster STREET: 2000 Pennsylvania Avenue,
FILING DATE:
                 APPLICATION NUMBER:
                                                                                                                                            ZIP:
                                                                                                                                                            COUNTRY:
                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 DKEAPQ~KSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 TRGLPKAKSHAP 245
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                                                                                                                                            20006-1888
                                                                                                                                                                                                Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGI 348
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27..43
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07-JUN-1995
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residue 132 of SEQ ID NO:2"
                                                                                                                                                                                                                                                                                           PROCESS FOR PRODUCTION OF INHIBITED FORMS OF ACTIVATED BLOOD FACTORS
             US/08/474,042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches
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                                                                                                                                                                                RESULT 96
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                                                                                                                       ; Sequence 3, Application US/08484558 ; Patent No. 5602233
                                                                                                                                                               US-08-484-558-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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TELEY: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
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                                                   APPLICANT: King, Robert TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   290 QAGQET-LYTGWGYHSSREKEAKKNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 RWEKWELDLDIKEVFVHDNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELN 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTL- 119
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Morrison & Foerster
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                                                                       PROCESS FOR PRODUCTION OF INHIBITED
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LENGTH: 254 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 28
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LOCATION:
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OTHER INFORMATION:
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234 TRGLPKAKSHAP 245
                                  409 DKEAPQ-KSWAP 419
                                                                      174 DTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGIYTKVTAFLKWIDRSMK 233
                                                                                                            349 LGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIR 408
                                                                                                                                                                                      290 QAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGI 348
                                                                                                                                                                                                                                                                 230 RWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELN 289
                                                                                                                                                                                                                                                                                                                                           170 LIDGKWTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLR 229
                                                                                                                                                                                                                            61 QEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLKLKTPITFRMNVAPACLPERDWAESTL- 119
                                                                                                                                                                                                                                                                                                       1 IVGGQECKDGECFWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTE 60
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(202)822-0168
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156..170
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residue 132 of SEQ ID NO:2"
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RESULT 97

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; Sequence 3, Application US/08774592 ; Patent No. 5770699
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Best Local Similarity 36.1%;
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TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBT
TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-Dec-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,978
FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION
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STREET: Z000
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LOCATION:
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                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Disulfide linkage with OTHER INFORMATION: residue 132 of SEQ ID NO:2"
                                                                                                                                                                                                                                                                                                                                              LOCATION: 108
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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230 RWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELN 289
                                                                                          170 LIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLR 229
                                                      1 IVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTE 60
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SYSTEM: PC-DOS/MS-DOS
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181..209
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156..170
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                                                                                                                                                19.9%; Score 463.5; DB 1; Length 254; 36.1%; Pred. No. 6e-32;
                                                                                                                              58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2803-0007.02
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US-08-330-978-4 RESULT 98

COUNTRY:

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Sequence 4, Application US/08330978 Patent No. 5589571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 28-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: King, Robert TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIB: TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,5
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                     OTHER INFORMATION: /note= "Disulfide linkage with CTHER INFORMATION: residue 132 of SEQ ID NO:2"
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
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Disulfide-bond
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27..43
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156..170
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US-08-474-042-4
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Patent No. 5589572
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APPLICANT: King,
                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,558
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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                                                FEATURE
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    NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                    TOPOLOGY: 1ii
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                                                                                                                                                                                                                                                                                                                                 NAME: Murashige, Kate H.
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                                                                                                              amino acid
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                                                                                                                                                                                                                          (202)822-0168
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  Disulfide-bond 7..12
                                                                       linear
                                                                                                                                                                                                                                               (202) 887-1500
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NAME/KEY:
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CATION:

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NAME/KEY:

NAME/KEY: LOCATION: FEATURE:

LOCATION: NAME/KEY:

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US-08-474-042-4
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US-08-484-558-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08484558 Patent No. 5602233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
              ATTORNEY/AGENT INFORMATION:
NAME: MUTABhige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)887-1500
                                                                                                                                                                                                                      ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: King, Robert
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED
TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS
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LOCATION:
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OTHER INFORMATION: /note= "Disulfide linkage with OTHER INFORMATION: residue 132 of SEQ ID NO:2"
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                                                                                                                           APPLICATION NUMBER: US/08/484,558
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
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181..209
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US-08-484-558-4
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Sequence 4, Application US/08774592
Patent No. 5770699
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ZIP: 2006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICANT: King, Robert TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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27..43
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                                  Version #1.30
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US-08-774-592-4
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                    Sequence 10, Application US/08558269 Patent No. 5961973 GENERAL INFORMATION:
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NAME/KEY:
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ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTATION NUMBER: 29,959
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APPLICANT: Crea, Roberto
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TELECOMMUNICATION INFORMATION:
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LOCATION:
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156..170
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residue 132 of SEQ ID NO:2"
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REFERENCE/DOCKET NUMBER: CXI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
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                                                                                                               GENERAL INFORMATION:
APPLICANT: Crea, 1
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION NUMBER: US 07/847,800
APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
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                                                     NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                               TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 60 50
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/558,269 FILING DATE: 13-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
CITY: Boston
                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 DTEDQEDQVD-------PRLIDGKWTRRGDSPWQVVLL-DSKKKLAC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 GAVLIHPSWVLTAAHCM-----DES----KKLLVRLGEYDLRRWBK-WELDLDIKEVFVHP 247
                                                                                                                                                                                                                                                                          325 PFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWI 367
                                                                                                                                                                                                                                                                                                                  363
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                                                                                                                                                                                                                                                                                                                                                                                                                               206 RYNWRENLDRDIALMKLKKPVAFSDYTHPVCLPDRETA-ASLLQAGYKGRVTGWGNLKET 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 NYS-KSTIDNDIALLHLAQPAILSQIIVPICLPDSGLAERELNQAGQEILVIGWG-YHSS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 EVEDQKEEVQLLVFGLTANSDTHLLHGQSLTLIVEGSDAEIGMSPWQVMLFRKSPQELLC 145
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                                                                                                                                                                                                                                                                                                                PMV--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                          REKEAKRNRIFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIL---GDRQDACEGDSGG 362
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                    60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                     LAHIVE & COCKFIELD
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                                                                                                                 Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 448; DB 2
36.7%; Pred. No. 2e-30;
Ltive 45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
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Best Local Similarity
                                                                                                                                                                                                                                  Sequence 52, Appli
Patent No. 6232456
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                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
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APPLICATION NUMBER: US/09/410,882
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: US 07/847,800
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TITLE OF INVENTION: TITLE OF INVENTION:
                                                          APPLICANT:
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                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: CRI-001CP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 GAVLIHPSWVLTAAHCM-----DES---KKLLVRLGEYDLRRWEK-WELDLDIKEVFVHP 247
                                                                                                                                                                                                                                                                                                                                                   325 PFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWI 367
                                                                                                                                                                                                                                                                                                                                                                                                                            265 WTANVGKGQPSVLQVVNLPIVERPVCKDSTRITIDNMFCAGYKPDEGKRGDACEGDSGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 RYNWRENLDRDIALMKLKKPVAFSDYIHPVČLPDRETA-ASILQAGYKGRVTGWGNLKET 264
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                                                                                                                                                                                                                                                                                                                                                                                      363 PMV--ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                Application US/08944483
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RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
STROUPE, STEVEN D.
VENTION: NOVEL SERINE PROTEASE REAGENTS
VENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
VENTION: OF THE PROSTATE
                                                                                                             FRIEDMAN, PAULA N. GRANADOS, EDWARD N. KLASS, MICHAEL R.
                                                                                                                                                                       COLPITTS, TRACEY L.
                                                                                                                                                                                              COHEN, MAURICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Mismatches
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                                                                                                               Sequence 49, Applicati
Patent No. 6232456
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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US-08-944-483-52
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NOMBER: US/08/944,483
APPLICATION NUMBER: US/08/944,483
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 19.1%; Score 444; DB 3; Length 259; Local Similarity 39.8%; Pred. No. 2.9e-30; pes 100; Conservative 41; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                   180 RITDNMFCAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGF 239
                                           393 YTKVSRYLDWI 403
                                                                                                                                 338 MVSENMLCAGIL---GDRQDACEGDSGGPMV--ASFHGTWFLVGLVSWGEGCGLLHNYGV 392
                                                                                                                                                                               121 PDRETA-ASILQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVVNLPIVERPVCKDSTRI 179
                                                                                                                                                                                                                          279 PDSGLAERELNQAGQETLYTGWG-YHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSN 337
                                                                                                                                                                                                                                                                                                                  221 VRLGEYDLRRWEK-WELDLDIKEVFVHPNYS-KSTTDNDIALLHLAQPATLSQTIVPICL 278
                                                                                                                                                                                                                                                                       61 VRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSDYTHPVCL 120
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YTHVFRLKKWI 250
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Application US/08944483

GRANADOS, EDWARD I KLASS, MICHAEL R. RUSSELL, JOHN C.

EDWARD N PAULA N. TRACEY L.

COLPITTS, FRIEDMAN, COHEN, MAURICE

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                    Sequence 1, Application US/08148910 Patent No. 5466593 GENERAL INFORMATION:
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ADDRESSEE: Abbott Laboratories
'STREET: 100 Abbott Park Road
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Takeshi SHIMOMURA et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 19.0%; Score 441; DB 3; Length 247; Local Similarity 35.3%; Pred. No. 4.9e-30; ses 89; Conservative 57; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                            117 -MTQKTGIVSGFGRTHEKGRQSTR-----LKMLEVPYVDRNSCKLSSSFIITQNMFCAGY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 RWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELN 289
                                                                                                                                                                       231 TRGLPKAKSHAP 242
                                                                                                                                                                                                             409 DKEAPQ-KSWAP 419
                                                                                                                                                                                                                                                                                             349 LGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIR 408
                                                                                                                                                                                                                                                                                                                                                                                    290 QAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNBCSEVMSNMVSENMLCAGI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                 58 QEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTL- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVGGOECKDGECPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRF---EGDRNTE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60064-3500
                                                                                                                                                                                                                                                       DTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGXYGIYTXVTAF1KWIDRSMK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEWART,
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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LENGTH: 300 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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OPERATING SYSTEM: MS-DOS
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MEDIUM TYPE: 500 Kb Storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                      108 YCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVD 167
                                                                                                                                                                                                                                     107 LGQHFFNRTTDVTQTFGIEKYIPYTLYSVFNPSDHDLVLIRLKKKGDRCATRSQFVQPIC 166
                                                                                                                                                                                                                                                                           223 LGEYDLRRWEKWELDLDIKEVFVHPNYSK-STTDNDIALLHLAQP----ATLSQTIVPIC 277
                                                                                                                                                                                                                                                                                                                                                          168 PRLIDGKWTRRGDSPW--QVVLLDSKKKLACGAVLIHPSWVLTAAHCMDES---KKLLVR 222
272 KPGVYTRVANYVDWINDRIR---PPRRLVAP 299
                             389 NYGVYTKVSRYLDWIHGHIRDXEAPQKSWAP 419
                                                                           212 CSSPEVYGADISPNMLCAGYFDCKSDACQGDSGGPLACEKNGVAYLYGIISWGDGCGRLH
                                                                                                              331 CS--EVMSNMVSENMICAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                          167 LPEPG-
                                                                                                                                                                                                278 LPDSGLAERELNQAGQETLVTGWGY-----HSSREKEAKRNRTFVLNFIKIEVVPHNE 330
                                                                                                                                                                                                                                                                                                                                                                                                  6 YCRLEA----CESLIRVQLSPDLLATLPEPASPGRQACGRRHKKRTFLR-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Mismatches 115;
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US-08-448-937A-1

RESULT 107

; Sequence 1, Application US/08448937A

Patent No. 5677164

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 5677164ember: 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/448,937A FILING DATE: May 24, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 5.25 inch, MEDIUM TYPE: 500 Kb Storage
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272 KPGVYTRVANYVDWINDRIR---PPRRLVAP 299
                                    389 NYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                     LPDSGLAERELNQAGQETLVTGWGY------HSSREKEAKRNRTPVLNFIKIPVVPHNE 330
                                                                                                                                                                                                                                                                                                                                 PRIIGGSSSLPGSHPWLAAIYIGDS----FCAGSLVHTCWVVSAAHCFSHSPPRDSVSVV 106
                                                                                                                                                                                                                                                                                                                                                                      PRLIDGKWIRRGDSPW--QVVLLDSKKKLACGAVLIHPSWYLTAAHCMDES---KKLLVR 222
                                                                                                                                                                                                                                                                                                                                                                                                                 YCRLEA----CESLTRVQLSPDLLATLPEPASPGRQACGRRHKKRTFLR---
                                                                                                                       CS--EVMSNMVSENMICAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLH 388
                                                                                                                                                                                                                                              LGQHFFNRTTDVTQTFGIEKYIPYTLYSVFNPSDHDLVLIRLKKKGDRCATRSQFVQPIC 166
                                                                                                                                                                LPEPG----STFPAGHKCQIAGWGHLDENVSGYSSSLREA------LVPLVADHK 211
                                                                              CSSPEVYGADISPNMLCAGYFDCKSDACQGDSGGPLACEKNGVAYLYGIISWGDGCGRLH 271
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805 Fifteenth Street, N.W., #700
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No. 5677164el Protein and Gene Encoding Said Protein
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.7%; Score 435; DB 3; Length 400; Best Local Similarity 32.0%; Pred. No. 2.9e-29; Matches 108; Conservative 45; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
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APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: FURNITION: FIEA PROTEASE PROTEINS, NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/004,731
APPLICATION NUMBER: US/09/004,731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
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358 MQIEGRRTLVGLVSWGIGCGREHLPGVYTNIQKFIPWI
                                                                                298 QSTVPAVLQEVDVEVIPNERCQRWFRAAGRRETIHDVFLCAGYKEGGRDSCQGDSGGPLI 357
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                                          366 ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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6177258
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                                                                                                                                                                                                                                                       GGALVSDRWVITAAHCVATTPNSNLKVRLGEWDVRDHDERLNHEEYAIERKE--VHPSYS 246
                                                                                                                                                                                                                                                                                             GAVLIHPSWVLTAAHCM--DESKKLLVRIGEYDLR----RWEKWELDLDIKEVFVHPNYS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKF 139
                                                                                                                                                                  PTDFRNDVALVKLDRTVIFKQHILPVCLP----HKQMKLAGKMATVAGWG----RTRHG 297
                                                                                                                                                                                                                                                                                                                                            TCGELYTRSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                CRYKGERFECGLSIS----CVLGGGKPLDLCSGGMIW---SCCVDRDIRPEPQHQGALQNA 147
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                                                                                                                          KRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILGDRQDACEGDSGGPMV 365
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                                                                                                                                                                                                                                                                                                                                              ----RIVGGHSTGFGSHPWQAALIKSGFLSKKLSC 188
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US-09-004-731-33
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APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
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ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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APPLICATION NUMBER:
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358 MQIEGRRILVGLVSWGIGCGREHLPGVYTNIQKFIPWI 395
                                    366 ASEHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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Denver

    Application US/09004731
6177258

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                                                                                  QSTVPAVLQEVDVEVIPNERCQRWFRAAGRRETIHDVFLCAGYKEGGRDSCQGDSGGPLI 357
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RESULT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 108; Conservative
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APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FILE PROTI
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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STATE:
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                                366 ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                 311 KRNRTFYLNFIKIFYVPHNECSEVM-----SNWVSENWLCAGILGDRQDACEGDSGGPMV 365
                                                                                                                                                                                                  251 KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEA 310
358 MQIEGRATLVGLVSWGIGCGREHLPGVYTNIQKFIPWI 395
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                                                                            QSTVPAVLQEVDVEVIPNERCQRWFRAAGRRETIHDVFLCAGYKEGGRDSCQGDSGGPLI 357
                                                                                                                                                             PTDFRNDVALVKLDRTVIFKOHILÞVCLÞ----HKOMKLÁGKMATVAGMG----RTRHG 297
                                                                                                                                                                                                                                                                  GAVLIHPSWVLTAAHCM--DESKKLLVRLGEYDLR----RMEKMELDLDIKEVFVHPNYS 250
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                                                                                                                                                                                                                                            GGALVSDRWVITAAHCVATTPNSNLKVRLGEWDVRDHDERLNHEEYAIERKE--VHPSYS 246
                                                                                                                                                                                                                                                                                                                                                                  PCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGDSPWQVVLLDS---KKKLAC 196
                                                                                                                                                                                                                                                                                                                                                                                                            CRYKGERFECGLSIS----CVLGGGKPLDLCSGGMIW----SCCVDRDIRPEPQHQGALQNA 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.7%; Score 435; DB 3; Length 400; 32.0%; Pred. No. 2.9e-29; ative 45; Mismatches 135; Indels
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                                                                                                                                                                                                                                                                                                                                RIVGGHSTGFGSHPWQAALIKSGFLSKKLSC 188
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RESULT 111
US-08-749-699-33
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RESULT 112
US-09-004-729-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 18.7%; Score 435; DB 3; Length 400; Best Local Similarity 32.0%; Pred. No. 2.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wu Hunter, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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CITY: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/749,699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                148 TCGELYTRSN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108; Conservative
                                                                                                                                                                                                                     311 KRNRTFYLNFIKIPYVPHNECSEVM-----SNMVSENMLCAGILGDRQDACEGDSGGPMV 365
                                                                                                                                                                                                                                                                                                             251 KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEA 310
                                                                                     358 MQIEGRRTLVGLVSWGIGCGREHLPGVYTNIQKFIPWI 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 CRYKGERFECGLSIS---CVLGGGKPLDLCSGGMIW---SCCVDRDIRPEPQHQGALQNA 147
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T: 1700 Lincoln Street, Suite 3500
Denver
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                                                                                                                                                                                                                                                                    PTDFRNDVALVKLDRTVIFKQHILEVCLE----HKQMKLAGKMATVAGWG----RTRHG 297
                                                                                                                               ASPHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                            GGALVSDRWVITAAHCVATTPNSNLKVRLGEWDVRDHDERLNHEEYAIERKE--VHPSYS 246
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Patent No. 6406900
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wu Hunter, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUT
TITLE OF INVENTION: MOLECULES AND USES THEREOF
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 400 amino acids TYPE: amino acid TOPOLOGY: linear
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ZIP: 80203
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                                                                                                                              311 KRNRTFYLNFIKIPYVPHNECSEVM-----SNMVSENMLCAGILGDRQDACEGDSGGPMV 365
                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                      140 PCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDS---KKKLAC 196
358 MQIEGRATIVGIVSWGIGCGREHLPGVYTNIQKFIPWI 395
                                                                                                                                                                                                                         251 KSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGWGYHSSREKEA 310
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                                                                                                                                                                                                                                                                                                                                                              148 TCGELYTRSN---
                                            366 ASFHGTWFLYGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 CRYKGERFECGLSIS---CVLGGGKPLDLCSGGMIW---SCCVDRDIRPEPQHQGALQNA 147
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                                                                                      QSTVPAVLQEVDVEVIENERCQRWFRAAGRRETIHDVFLCAGYKEGGRDSCQGDSGGPLI 357
                                                                                                                                                                             PTDFRNDVALVKLDRTVIFKOHILPVCLP-----HKOMKLAGKMATVAGWG-----RTRHG 297
                                                                                                                                                                                                                                                                     GGALVSDRWVITAAHCVATTPNSNLKVRLGEWDVRDHDERLNHEEYAIERKE--VHPSYS 246
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1700 Lincoln Street, Suite 3500
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US-09-004-729-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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STATE: Colora
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358 MQIEGRRILVGLVSWGIGCGREHLPGVYTNIQKFIPWI 395
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                                                                                366 ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                                                                                                                                                                                  311 KRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILGDRQDACEGDSGGPMV 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 GAVLIHPSWVLTAAHCM--DESKKLLVRLGEYDLR----RWEKWELDLDIKEVFVHPNYS
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Stiegler, Gary
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Patent No. 6204010
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TITLE OF INVENTION: FILE PROTESSE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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                                 366 ASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                            285 QSTVPAVLQEVDVEVIPNERCQRWFRAAGRRETIHDVFLCAGYKEGGRDSCQGDSGGPLT 344
                                                                                                                    311 KRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILGDRQDACEGDSGGPMV 365
                                                                                                                                                            234 PTDFRNDVALVKLDRTVIFKOHILEVCLP----HKQMKLAGKMATVAGWG----RTRHG 284
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345 MQIEGRRTLVGLVSWGIGCGREHLPGVYTNIQKFIPWI 382
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    amino acid
XY: linear
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(707 Th NO: 8:
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                             -RIVGGHSTGFGSHÞWQAALIKSGFLSKKLSC 175
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US-09-032-215-13
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Patent No. 620401
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Best Local Similarity 32.0%;
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LENGTH: 387 amino acids
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APPLICATION NUMBER: US/09/032,215
FILING DATE: 27-FEB-1998
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ADDRESSEE: Sheridan Ross P.C.
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APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FILE PROTEASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII DOS TEXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                             311
                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                   197 GAVLIHPSWVLTAAHCM--DESKKLLVRLGEYDLR----RWEKWELDLDIKEVEVHPNYS 250
                                                                                                                                                                                                                                                                                                                                                                                        140 PCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGDSPWQVVLLDS---KKKLAC 196
345 MQIEGRRTLYGLYSWGIGCGREHLPGYYTNIQKFIPWI 382
                                                                                    285
                                                                                                                                                                        234 PTDFRNDVALVKLDRTVIFKQHILPVCLP----HKQMKLAGKMATVAGWG----RTRHG 284
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                                                                                                                                                                                                                                                                                                                                                 135 TCGELYTRSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 CRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKF 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CRYKGERFECGLSIS---CVLGGGKPLDLCSGGMIW---SCCVDRDIRPEPQHQGALQNA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colorado
                                    ASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
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                                                                                  QSTVPAVLQEVDVEVIPNERCQRWFRAAGRRETIHDVFLCAGYKEGGRDSCQGDSGGPLT 344
                                                                                                                               KRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAGILGDRQDACEGDSGGPMV 365
                                                                                                                                                                                                             KSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEA 310
                                                                                                                                                                                                                                                             GGALVSDRWVITAAHCVATTPNSNLKVRLGEWDVRDHDERLNHEEYAIERKE--VHPSYS 233
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) NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Mismatches 136; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 432; DB 3; Length 387; Pred. No. 5e-29;
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                                                                                                                                                                                                                                                                                                                                                   -RIVGGHSTGFGSHPWQAALIKSGFLSKKLSC 175
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US-08-944-483-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICATION NAMES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
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TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 LIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLR 229
    171
                                                                                                                                                                                                                                                                                                                                                                              230 RWEKWELDLDIKEVFVHPNYSKSTT--DNDIALLHLAQPATLSQTIVPICLPDSGLAERE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VVGGEDAKPGQFPWQVV-LNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVAGEHNIE
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AGFHEGGRDSCOGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRYVNWI 228
                                                                        AGILGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWI 403
                                                                                                                                                     LKFG--SGYVSGWGRVFHKGRS-----ALVLQYLRVFLVDRATCLRSTKFTIYNNWFC 170
                                                                                                                                                                                                                                                                                                      ETEHTEOKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADKEYTNIF 119
                                                                                                                                                                                                                         LNQAGQETLVTGWG--YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLC 345
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100 Abbott Park Road
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STEWART, KENT D.
STROUPE, STEVEN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLASS, MICHAEL R.
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RESULT 117
US-09-004-731-36
RESULT 118
US-08-749-699-36
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Best Local Similarity
Matches 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wu Hunter, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID TITLE OF INVENTION: MOLECULES AND USES THEREOF NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palanne
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STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/004,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                  118 ----HKQMKLAGKMATVAGWG----RTRHGQSTVPAVLQEVDVEVIPNERCQRWFRAAGR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 LIDGKWIRRGDSFWQVVLLDS---KKKLACGAVLIHPSWVLTAAHCM--DESKKLLVRLG 224
                                                                                      230 IQKFIPWI 237
                                                                                                                                396 VSRYLDWI 403
                                                                                                                                                                            170 RETIHDVFLCAGYKEGGRDSCQGDSGGPLIMQIEGRRTLVGLVSWGIGCGREHLPGVYTN 229
                                                                                                                                                                                                                   336 SNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLYGLYSWGEGCGLLHNYGYYTK 395
                                                                                                                                                                                                                                                                                                         281 SGLAERELNQAGQETLVTGWGYHSSREKEAKRIRTFVLNFIKIPVVPHNECSEVM----- 335
                                                                                                                                                                                                                                                                                                                                                                                                  225 EYDLR----RWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPD 280
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                                                                                                                                                                                                                                                                                                                                                   61 EWDVRDHDERLNHEEYAIERKE--VHPSYSPTDFRNDVALVKLDRTVIFKQHILFYCLP- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGHSTGFGSHPWQAALIKSGFLSKKLSCGGALVSDRWVITAAHCVATTPNSNLKVRLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%; Score 428.5; DB 3; Length 242; 37.1%; Pred. No. 5.6e-29; tive 40; Mismatches 91; Indels 25;
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Patent No. 6406900
GENERAL INFORMATION:
APPLICANT: Wu Hunts
APPLICANT: Stiegle:
APPLICANT: Gaines,

Stiegler, Gary Gaines, Patrick J. Wu Hunter,

Shirley

US-09-004-729-36

Sequence 36,

Application US/09004729

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gaines, Fatrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 18.4%; Score 428.5; DB 3; Local Similarity 37.1%; Pred. No. 5.6e-29; hes 92; Conservative 40; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sheridan Koss r.c. STREET: 1700 Lincoln Street, Suite 3500
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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                                       396 VSRYLDWI 403
                                                                               170 RETIHDVFLCAGYKEGGRDSCQGDSGGPLIMQIEGRRTIVGLVSWGIGCGREHLPGVYTN 229
                                                                                                                     336 SNWVSENMICAGIIGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTK 395
                                                                                                                                                               118 ----HKOMKLAGKMATVAGWG----KTRHGOSTVPAVLQEVDVEVIPNERCQRWFRAAGR 169
                                                                                                                                                                                                       281 SGLAERELNOAGQETLYTGWGYHSSREXEAKRNRTFYLNFIKIPVVPHNECSEVM----- 335
                                                                                                                                                                                                                                                                                            225 EYDLR----RWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPD 280
230 IQKFIPWI 237
                                                                                                                                                                                                                                                  61 EWDVRDHDERLNHEEYAIERKE--VHPSYSPTDFRNDVALVKLDRTVIFKOHILPVCLP- 117
                                                                                                                                                                                                                                                                                                                                    1 IVGGHSTGFGSHFWQAALIKSGFLSKKLSCGGALVSDRWVITAAHCVATTPNSNLKVRLG 60
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US-09-004-729-36
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                                                                                                                                             Sequence 1, Application US/08750711 Patent No. 5741771
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                                                                                                                                           Patent No.
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INFORMATION FOR SEQ ID NO: 36:
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                          APPLICANT: Dawson, Keith M
APPLICANT: Wood, Lars M
APPLICANT: Comer, Michael B
CORRESPONDENCE ADDRESS:
                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palantin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 LIDGKMTRRGDSPWQVVLLDS---KKKLACGAVLIHPSWVLTAAHCM--DESKKLLVRLG 224
                                                                                                                                                                                                                                                                                                                                                   170 RETIHDVFLCAGYKEGGRDSCQGDSGGPLIMQIEGRRTLVGLVSWGIGCGREHLPGVYTN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 SGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----
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                                                                                                                                                                                                                                                                    230 IQKFIPWI 237
                                                                                                                                                                                                                                                                                                             396 VSRYLDWI 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ----HKQMKLAGKMATVAGWG----RTRHGQSTVPAVLQEVDVEVIPNERCQRWFRAAGR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWDVRDHDERLNHEEYAIERKE--VHPSYSPTDFRNDVALVKLDRTVIFKQHILPVCLP- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLEA PROTEASE PROTBINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                        THROMBOLYTIC COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103
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                                                                                                                                             RESULT 121
US-08-944-483-63
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                                                                                                       ; Sequence 63, Application US/08944483; Patent No. 6232456
                                                                                      GENERAL INFORMATION:
    APPLICANT:
APPLICANT:
APPLICANT:
                                                                  APPLICANT:
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COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N. COHEN, MAURICE

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US-08-750-711-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: HOSCHEIT, DALE H.
REGISTRATION UNBER: 19,090
REFERENCE/DOCKET NUMBER: 1018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHAX: 202-508-9200
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Banner & Allegretti, Ltd. STREET: 1001 G Street, N.W. CITY: Washington, D.C. STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                  668 KDIALLKLSSPAVITDKVIPACLPSPNYVVADR-----TECFITGWG-------BTQ 712
                                                                                                                                                                                                                                                                           614 TLISPEWVLTAAHCLKKSPRPSSYKVILGAHQKVNLEPHVQEIEVSRLFLEP-----TR 667
                                                                                                                                                                                                                                                                                                                       199 VLIHPSWYLTAAHCMDESKK---LLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTD 255
                                                                                                                                                                                                                                                                                                                                                                                                                  139 FPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                523 RAGLEKNYCR-----NPDGDVGG-----PW--CYTTNPRKLYDYCDVPQC-AAPS 564
                                                                                         713 GTRGAGLLKEAQLÞVIENKVCNRYEFLNGRVQSTELCÁGHLAGGTDSCQGDSGGÞLVCFE 772
                                                                                                                                    314 RTFVLNFIK---IPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASF 368
                                                                                                                                                                                                                           256 NDIALLHLAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWGYHSSREKEAKRN 313
773 KDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRN 813
                                           369 HGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 RSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGD--DLLQCHPAVK 138
                                                                                                                                                                                                                                                                                                                                                                       FDCGKP--QVEPKKCTTK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10180.01675
                                                                                                                                                                                                                                                                                                                                                                            --IKPRIVGGCVAHPHSWPWQVSLRTRFGMHFCGG 613
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; Sequence 3, Application US/08681151; Patent No. 5869637
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                                RESULT 122
US-08-681-151-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RISSEL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, STEVEN D.
APPLICANT: STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Becker Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                170 LIDGKWIRRGDSPWQV----VILDSKKKILACGAVLIHPSWVILTAAHCMDESKKILLVRLIGEY 226
                                                                                                       224
                                                                                                                                                                                                                                                   113 CLPSKG----DISTIYINCWVIGWGF--SKEKGEIQN---ILQKVNIPLVINEECQKRYQ 163
                                                                                                                                         396 VSRYLDWI 403
                                                                                                                                                                             164 DYKITORMYCAGYKEGGKDÁCKGDŚGGPLVCKHNGMWRLVGITSWGEGCARREQPGVYTK 223
                                                                                                                                                                                                                                                                                     277 CLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSE-VM 335
                                                                                                                                                                                                                                                                                                                                                            227 DLRRWEKWELDL----
                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGTNSSWGEWPWQVSLQVKLTAQRHL-CGGSLIGHQWVLTAAHCFD------GLPLQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I: 248 amino acids amino acid
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                                                                                                                                                                                                               SNMVSENWICAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTK 395
                                                                                                                                                                                                                                                                                                                          DVWRIYSGILNLSDITKDTPFSQIKEIIIHQNYKVSEGNHDIALIKLQAPLNYTEFQKPI 112
                                                                                                         VAEYMDWI 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Mismatches
                                                                                                                                                                                                                                                                                                                                                          ---DIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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                                                                                                                                                                                                                                                                                                                                                                  190
     464 SSİKELIIHQKYKMSEGSYDİALIKLQTPLNYTEFQKPİCLP----SKADTNTIYTNCWV 519
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 638 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Braxton, Scott Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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SOFTWARE: FastSEC
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TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             239 ----FFTFYTNEWETE-SQRNVCFLKTS-KSGRPSPPIIQENAVSGYSLFTCRKARPEP 291
239 -DIKEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERBLNQAGQETLV 297
                                                412 LVSQNHM-CGGSIIGRQWILTAAHCFD-----GIPYPDVWRIYGGILNLSBITNKTPF 463
                                                                                            188 LDSXKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDL------
                                                                                                                                       352 STDGSPTRITYEAQGSSGYSLRLCKVVESSDCTTKINARIVGGTNSSLGEWPWQVSLQVK 411
                                                                                                                                                                                                                                 292 CHFKIYSGVAFEGEELNATFVQGADACQETCTKTIRCQFFTYSLLPQDCKAEGCKCSLRL 351
                                                                                                                                                                                                                                                                                                                                                                         71 DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEE---VGWRRCSCA----- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 SLERECIEEI-CDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCCGHGTCI 70
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                                                                                                                                                                                                                                                                                  ----PGYKLGDDLLQCHPAVKFPCGRPWK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.8%; Score 414; DB 2; Length 638; 28.3%; Pred. No. 3.2e-27; ative 66; Mismatches 159; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 110;
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RESULT 123
US-08-248-629A-1
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                                                                                                                                                                                                                                                                                                                                                                              Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LAIRY W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 052
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: MacIntosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 TGWGYHSSREKEAKRNRTEVLNFIKIPVVPHNECSEVMSN-MVSENMLCAGILGDRQDAC 356
                                         673
  316 FVLNFIKIPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWF 373
                                                                                                                         624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
                                                                                                                                                                 211 HCMDESKK---LLVRIGEYDLRRWEKWELDLDIKEVFV-----HPNYSKSTIDNDIALLH 262
                                                                                                                                                                                                                                                  160 EDQEDQVDP-----RLIDGKWTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                                                                            529 NYCRNEDGDVNGEW--CYTTNERKLYDYCDIFLCASASSFECGKP------
                                                                                                                                                                                                                                                                                                                                    107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWXRMEKKRSHLKRDT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atlanta
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                                                                                                                                                                                                           -----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRFTGQHFCGGTLIAPEWVLTAA 623
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                                         LSRPATITOKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA-----
                                                                               LAQPATISQTIVPICLPDSG--LAERELNQAGQETLVTGWG----YHSSREKEAKRNRT 315
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                                                                                                                                                                                                                                                                                                                                                                                                  17.7%; Score 412; DB 1; Length 812; 32.1%; Pred. No. 6.3e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 08/248,629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method of Treating an Anglogenic TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Folkman, Judah APPLICANT: O'Reilly, Mich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LATTY W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0123
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/451,932 FILING DATE: 05/26/95
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316 FVLNFIKIPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGEMVASFHGTWF 373
                                                                                                                                                    624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
                                                                                                                                                                                           211 HCMDESKK---LLVRLGEYDLRRWEKWELDLDIKEVFV-----HPNYSKSTTDNDIALLH 262
                                                                                                                                                                                                                                   572 ----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRETGQHFCGGTLIAPEWVLTAA 623
                                                                                                                                                                                                                                                                             160 EDQEDQVDP-----RLIDGKMTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                                                                                                       529 NYCRNPDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP--
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                                                                  LSRPATITDKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA----- 721
                                                                                                       LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
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RESULT 125
US-08-452-260-1
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Patent No. 5776704
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Method of Diagnosing an Angiogenic
TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 812
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APPLICATION NUMBER: 08/2-
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0124
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FILING DATE: 05/26/95
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                                316 FVLNFIKIPVVPHNECS--EVMSNMVSENWLCAGILGDRQDACEGDSGGPMVASFHGTWF 373
                                                                                                                                                                                                                                                                                                                                                                                                    107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDT 159
                                                                                                                              263 LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
                                                                                                                                                                          624 HCLEKSSRPEFYKVILGAH----EBYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
                                                                                                                                                                                                                  211 HCMDESKK---LLVRIGEYDLRRWEKWELDLDIKEVFV----HPNYSKSTTDNDIALLH 262
                                                                                                                                                                                                                                                                 572 -----OVEPKKCPGRVVGGCVANPHSWPWQISL---RTRFTGQHFCGGTLIAPEWVLTAA 623
                                                                                                                                                                                                                                                                                                             160 EDQEDQVDP-----RLIDGKWIRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                                                                                                                                          529 NYCRNEDGDVNGEW--CYTTNERKLYDYCDIELCASASSFECGKE--------
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----QLPVIENKVCNRVEYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLVCFEKDKYI 775
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US-08-326-785-1
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GENERAL INFORMATION:
APPLICANT: FOLKMAN, Judah
APPLICANT: O'Reilly, Michael
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin and Method of Use
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Patent No. 5792845
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 04/26/94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: Microsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 LVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      776 LOGVISWGLGCARPNKPGVYVRVSRFVDWIEREMRN 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDT 159
                                                                                                                                                                                                                                                                                                                                                                                                        529 NYCRNPDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP------ 571
       374 LVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                      316 FVLNFIKIPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWF 373
                                                                                                                                     673 LSRPATITDKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA-----
                                                                                                                                                                             263 LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
                                                                                                                                                                                                                         624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
                                                                                                                                                                                                                                                                     211 HCMDESKK----LLVRLGEYDLRRWEKWELDLDIKEVFV-----HPNYSKSTTDNDIALLH 262
                                                                                                                                                                                                                                                                                                               572 -----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRFTGQHFCGGTLIAPEWVLTAA 623
                                                                                                                                                                                                                                                                                                                                                            160 EDQEDQVDP-----RLIDGKMTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108;
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                                                 --QLPVIENKYCNRVEYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLVCFEKDKYI 775
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32.1%;
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s; Pred. No. 6.3e-27;
51; Mismatches 91
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US-08-612-788-1
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                                                                                                                                                                                                                                                                                                 Matches 108;
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                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yihai APPLICANT: Sim, B. Kim Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Angiostatin Pragments and Method of Use NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO TYPE: N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/612,788
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                                                                                                                                                                                                                                                                                                                 / Match 17.7%; Score 412; DB 2; Length 812;
Local Similarity 32.1%; Pred. No. 6.3e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 812 amino acids
673 LSRPATITDKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA-----
                               263 LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG----YHSSREKEAKRNRT 315
                                                                    624
                                                                                                                                                                                 160 EDQEDQVDP-----RLIDGKMTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                                         107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDT 159
                                                                                                                                             572 -----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRFTGQHFCGGTLIAPEWVLTAA 623
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                                                                      HCLEKSSRPEFYKVILGAH---
                                                                                                      HCMDESKK----LLVRLGEYDLRRWEKWELDLDIKEVFV-----HPNYSKSTTDNDIALLH 262
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No
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                                                                                                                                                                                                                                                                                               51; Mismatches 91; Indels 86; Gaps
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                                                                    --EEYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
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Patent No. 586
                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.7%; Score 412; DB 2; Length 812; Best Local Similarity 32.1%; Pred. No. 6.3e-27;
                                                                                                                                                                                                                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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ZIP: 30303-1769
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REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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673 LSRPATITOKVIPACLPSPNYMVADRTI-----CYITGWGETQGTPGAGRIKEA----- 721
                                                                                                                                                                        572 -----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRFTGQHFCGGTLIAPEWVLTAA 623
                                                                                                                                                                                                                                                               529 NYCRNPDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP---
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                                       263 LAQPATLSQTIVPICLPDSG--LABRELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
                                                                                     624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN---
                                                                                                                            211 HCMDESKK----LLVRLGEYDLRRWEKWELDLDIKEVFV-----HPNYSKSTTDNDIALLH 262
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O'Reilly, Michael S.
NVENTION: Aggregate Angiostatin and Method of Use
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191 Peachtree Street, 37th Floor
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Patent No. 5885795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                             Matches 108;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Angiostatin and Method of Use NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
APPLICANT: Sim, Kim Lee
APPLICANT: Cao, Yihai
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                                                                                                                                                                                                                                                                                 HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,529
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S. ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                              ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 FVLNFIKIPVVPHNECS--EVMSNKVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 LVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
572 -----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRFTGQHFCGGTLIAPEWVLTAA 623
                                    160 EDQEDQVDP-----RLIDGKWTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                              529 NYCHNEDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP-
                                                                                                                  107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QLPVIENKVCNRVEYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLVCFEKDKYI 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQGVTSWGLGCARPNKPGVYVRVSRFVDWIEREMRN 811
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                                                                                                                                                                                                                                                                                                                                                                                                        812 amino acids
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                        17.7%; Score 412; DB 2; Length 812; 32.1%; Pred. No. 6.3e-27; tive 51; Mismatches 91; Indels
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US-08-866-735-1
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                                                                        Matches 108;
                                                                                                           Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                 IMMEDIATE SOURCE:
CLONE: Plasminogen
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                           Local
                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 FVLNFIKIPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASEHGTWF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 LSRPATITDKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 LAQPATLSQTIVEICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
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                               107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHEAVKEECGRPWKRMEKKRSHLKRDI 159
529 NYCRNPDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP----
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                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                     amino acid
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191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                          812 amino acids
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                                                                        Conservative
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                                                                                                                                                                                                                                                                         NO protein
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                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-1997
                                                                      17.7%; Score 412; DB 2; 32.1%; Pred. No. 6.3e-27; ative 51; Mismatches 91
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                                                                                                             Length 812;
                                                                              Indels
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US-09-066-028-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                      HYPOTHETICAL:
                                                                                                                                        MOLECULE TYPE:
IMMEDIATE SOURCE:
CLONE: Plasminogen
                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05
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                                           ORGANISM:
                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warren, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                      LENGTH: 812 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
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191 Peachtree Street,
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                                                                                                     NO
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                                                                                                                      : protein
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: mouse plasminogen US-09-192-012-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09192012A
Patent No. 6475784
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Inhibition of Angiogenesis by Delivery of Nucleic Acids TITLE OF INVENTION: Encoding Anti-Angiogenis Polypeptides FILE REFERENCE: 018484-000110US CURRENT APPLICATION NUMBER: US/09/192,012A CURRENT FILING DATE: 1998-11-13 EARLIER APPLICATION NUMBER: US 60/066,020 ERRLIER FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                 Matches 108;
                                                                                                                                                                                                                                                                                                                                                     Query Match 17.7%; Score 412; DB 4; Length 812; Best Local Similarity 32.1%; Pred. No. 6.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Papkoff, Jackie APPLICANT: Megabios Corporation APPLICANT: Pfizer, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 812
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 FVLNFIKIPYVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASEHGTWF 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 ----QVEPKKCPGRVVGGCVANPHSWPWQISL---RTRETGQHFCGGTLIAPEWVLTAA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 EDQEDQVDP-----RLIDGKWTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 NYCRNPDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP----
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                                                                                                                                                                                                                                                                                  107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDI 159
263 LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
                                              624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
                                                                                        211 HCMDESKK---LLVRLGEYDLRRWEKWELDLDIKEVFV-----HPNYSKSTTDNDIALLH 262
                                                                                                                                                                                    160 EDQEDQVDP-----RLIDGKNTRRGDSPWQVVLLDSKKKLA----CGAVLIHPSWVLTAA 210
                                                                                                                                                                                                                                     529 NYCRNPDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QLPVIENKVCNRVEYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLVCFEKDKYI 775
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                                                                                                                                          ----QVEPKKCPGRVVGGCVANPHSWPWQISI---RTRFTGQHFCGGTLIAPEWVLTAA 623
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                   51; Mismatches
                                                                                                                                                                                                                                                                                                                                   91;
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                                                                                                                                                               US-09-335-325-1
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Patent No. 6521439
GENERAL INFORMATION:
                                                                               Matches
                                                                                                                    Query Match
                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/335,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/612,788 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
                                                                                                                                                                                   CLONE: Plasminogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                    107 HYCLEEVG-----WRRCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDT 159
    529 NYCKNEDGDVNGPW--CYTTNPRKLYDYCDIPLCASASSFECGKP-
                                                                               108;
                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 812 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-Jun-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                             ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 30303-1769
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                                                                                                                                                                                                        CLONE:
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                                                                             17.7%; Score 412; DB 4; Length 812; 32.1%; Pred. No. 6.3e-27; tive 51; Mismatches 91; Indels
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US-08-991-761A-12
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                                                                                                                                                            ; MOLECULE TYPE: protein US-08-991-761A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6576609
GENERAL INFORMATION:
                                                                                 Matches 108;
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gately, Stephen
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: "Methods and Compositions for Generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: "Methods and TITLE OF INVENTION: Angiostatin"
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                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 FVLNFIKIPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWF 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 LVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   722 ----QLPVIENKVCNRVEYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLVCFEKDKYI 775
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529 NYCRNEDGDVNGPW--CYTTNERKLYDYCDIELCASASSFECGKE
                                    107 HYCLEEVG-----WERCSCAPGYKLGD--DLLQCHPAVKFPCGRPWKRMEKKRSHLKRDT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80203
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                                                                                                                                                                                                                                                                  812 amino acids
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                                                                                 Conservative
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                                                                                                  17.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/991,761A
                                                                               %; Score 412; DB 4; I
%; Pred. No. 6.3e-27;
51; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                            3501-16-1
                                                                                                                         Length 812;
                                                                                     Indels
                                                                                       86;
                                                                                     Gaps
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RESULT 135
PCT-US95-05107-1
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Applicant: The CH

Applicant: The CH

Applicant CHURNION
                                                                                                          PCT-US95-05107-1
         Query Match 17.7%; Score 412; DB 5; Length 812; Best Local Similarity 32.1%; Pred. No. 6.3e-27; Matches 108; Conservative 51; Mismatches 91; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION TITLE OF INVENTION: Angiostatin and Method of Use
                                                                                                                                                   MOLECULE TYPE: PI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Johnson, James D. REGISTRATION NUMBER: 31,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/05107
                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 LVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 FYLNFIKIPYVPHNECS--EVMSNMYSENMLCAGILGDRQDACEGDSGGPMVASFHGTWF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 LSRPATITOKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA----- 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 LAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWG-----YHSSREKEAKRNRT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN-----NRDIALLK 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   776 LOGVISWGLGCARPNKPGVYVRVSRFVDWIEREMRN 811
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                                                                                                                                                                                                                                                                                                                                                                404-818-3799
                                                                                                                                  Murine
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US-09-079-970A-5
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                                                                                                                                                               US-09-079-970A-5
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                                                                 Matches
                                                                   Best Local Similarity 35.0 Matches 92; Conservative
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         TELEFAX: (608) 831-210
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Niles, Andrew L. APPLICANT: Haak-Frendscho, Mary
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34!
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 53717-1914
                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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                                                                                                                                                                                                                                                      LENGTH: 249 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624 HCLEKSSRPEFYKVILGAH-----EEYIRGLDVQEISVAKLILEPN-----NRDIÄLLK 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 HCMDESKK----LIVRLGEYDLRRWEKWELDLDIKEVFY-----HPNYSKSTTDNDIALLH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572 ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              776 LQGVTSWGLGCARPNKPGVYVRVSRFVDWIEREMRN 811
----QLPVIENKVCNRVEYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLVCFEKDKYI 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSRPATITOKVIPACLPSPNYMVADRTI-----CYITGWGETQGTFGAGRLKEA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maffitt, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QVEPKKCPGRVVGGCVANPHSWPWQISi---RTRFTGQHFCGGTLIAPEWVLTAA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intellectual Property Department
                                                                                                                                                                                                                                                                                                                                                  (608) 831-2100
                                                                                                                                                                                                                                                                                                                          831-2106
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                                                                                           17.7%; Score 410.5; DB 35.0%; Pred. No. 2e-27;
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                                                                        42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  34506.073
                                                                                                                      DB 3;
                                                                          96;
                                                                               Indels
                                                                                                                        Length 249;
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                                                                               Gaps
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                                                                                                                                 US-08-469-486-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54,
                                                     Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Paul T. Clark REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version SOFTWARE: #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                          TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TLPPAS----ETFPPGMPCWVIGWG---DVDNDERLPPPFPLKQVKVPIMENHICDAKYH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 LLVRLGEYDLRRWEKWELD--LDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 NRPGIYTRVTYYLDWIHHYVPKK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 HNYGVYTKVSRYLDWIHGHIRDK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 LGAYTGDDVRIVRDDMLCAG--NTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 -----NMVSENMICAGILGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 CLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 DLAAL-RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVXVSSHVHTV 114
81 RSGWEGRFCQREVSF1NCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGD--DLLQCHPAVK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02110-2804
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                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEKRIVGGQEAPRSKWPWQVSL-----RVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08469486
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Holtet, Thor Las
Etzerodt, Michael
                                                                                                                                                                                                                             790 amino acids
                                                                                                                                                                                                                                                                                                               617 542 8906
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                                                         Conservative
                                                                                                                                                                          linear
                                                     17.6%; Score 410; DB 1; Length 790; 31.8%; Pred. No. 9e-27; tive 47; Mismatches 113; Indels 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Improved method for the refolding of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
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                                                           Gaps
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US-08-469-658-54
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                                       US-08-469-658-54
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GENERAL INFORMATION:
    Query Match
                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: Upper 5, FILING DATE: June 5, CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                TOPOLOGY:
                                                                                                  TYPE: amino STRANDEDNESS
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                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               545 FDCGKP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 RAGLEKNYCR-----NPDGDVGG------PW--CYTTNPRKLYDYCDVPQC-AAPS 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744 LVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRN 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 KSTTDNDIALLHLAQPATLSQTIVPICLPDSG--LAERBINQAGQETLVTGWGYHSSREK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 MVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 --BTQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGP 743
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                                                                                                                     amino acid
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Etzerodt, Michael
VENTION: IMPROVED METHOD FOR THE REFOLDING
VENTION: PROTEINS
                                                                                                                                       790 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                     617 542 8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 5, 1995
        17.6%;
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        Score 410;
                                                                                                                                                                                                                                                                                 06363/002002
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        DB 2;
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Length 790;

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RESULT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 03-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                             FILING DATE: 06-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Con
OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                          TOPOLOGY:
                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 40,943
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/131,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
  DESCRIPTION:
                                                                                                                                                                            TELEFAX: 847-938-2623
                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 -- ETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGP 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 EAKRNRTFVLNFIK---IPVVPHNECS--EVMSNMVSENMLCAGILGDRODACEGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      642 ---TRKDIALIKLSSPAVITDKVIPACLPSPNYVVADR-----TECFITGWG----- 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 KSTTDNDIALLHLAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWGYHSSREK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 LVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRN 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60064
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                                                               amino acid
                                                                                                                                                                                                                                                                                          Casuto, Dianne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Abbott Park Road
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                                                                                      791 amino acids
                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
protein
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NOVEL ANTIANGIOGENIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                           08/643,219
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                                                                                                                                                                                                                                                5940.US.P1
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Best Local Similarity 31.8%; Pred. No. 9e-27;
Matches 110; Conservative 47; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08832087B
Patent No. 5981484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                             INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6.
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Davidso: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60064
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: AND METHODS FOR INHIBITING
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acid
                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 59
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Abbott Park
                                                                                                                                     TELEX:
                                                                                                                                                            TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Abbott Laboratories
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643
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US-09-132-154-1
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Patent No. 6251867
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Best Local Similarity 31.8%;
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               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60064
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                               NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
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                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/643,219 FILING DATE: 06-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                              TELEPHONE:
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                                                                                                              847-938-3137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 410; DB 2; Length 791; Pred. No. 9e-27;
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US-08-991-761A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08991761A Patent No. 6576609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V¢
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,761A
FILING DATE:
CLASSIFICATION: 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                          TELEPHONE: (303) 863-97/
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: "Methods and Compositions for Generating
TITLE OF INVENTION: Angiostatin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                           REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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TOPOLOGY:
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                    LENGIH:
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                                                                                                                                                                                                                                                                                                          US/08/991,761A
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                                                                      <u>ه</u>
                                                                                                                                                                  3501-16-1
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                                                                                                                                                                                                                                                                                                                                                               Version #1.30
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RESULT 143
US-07-854-603-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5637
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                                                  INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
           SEQUENCE CHARACTERISTICS: LENGTH: 810 amino acid
                                                                                                       REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: McDonnell, John J
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: IC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: anti-thrombotic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Activatable fibrinolytic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: IL
COUNTRY: USA
                                                                                    TELEFAX:
                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 RAGLEKNYCR-----NPDGDVGG-----PW--CYTTNPRKLYDYCDVPQC-AAPS 545
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TRKDIALLKLSSPAVITDKVIPACLPSPNYVVADR----TECFITGWG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/07854603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Dr. John J. McDonnel
Ten South Wacker Drive, Suite 3000
                                                                                      312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forman, Joan M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edwards, Richard M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dawson, Keith M
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31.8%; Pred. No. 9e-27;
                                                                                                                                                                              John J
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                                                                                                                                                                                                                                                          US/07/854,603
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                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-854-603-2
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Patent No. 5688664
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                        APPLICATION NUMBER: US 07/854,603
FILING DATE: June: 4, 1992
APPLICATION NUMBER: GB 92 22758.6
FILING DATE: October 29, 1992
APPLICATION NUMBER: PCT/GB90/01912
FILING DATE: December 7, 1990
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Gilbert, Richard J
TITLE OF INVENTION: THROMBIN ACTIVATABLE PLASMINOGEN ANALOGUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/147,000B FILING DATE: October 29, 1993 CLASSIFICATION: 435
                                                                                                        NAME: Hoscheit, Dale H. REGISTRATION NUMBER: 19,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 LACGAVLIHPSWVLTAAHCMDESKK---LLVRLGEYDLRRWEKWELDLDIKEVFVHENYS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 FDCGKP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 EAKRNRTFVLNFIK---IPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACBGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 ---TRKDIALLKLSSPAVITDKVIPACLPSPNYVVADR-----TECFITGWG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 KSTTDNDIALLHLAQPATLSQTIVPICLPDSG--LAERBLNQAGQETLVTGWGYHSSREK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 HFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLPLEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    764 LVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIBGVMRN 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 MVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ETQGTFGAGLLKEAQLÞVIENKVCNRYEFLNGRVQSTELCÁGHLAGGTDSCQGDSGGÞ 763
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202-508-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-09-086-514-1
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                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 810
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                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PROTEIN HAVING A VASCULARIZATION INHIBITORY EFFECT AND TITLE OF INVENTION: A METHOD FOR PRODUCTION THEREOF AND A METHOD FOR TITLE OF INVENTION: PRODUCING ANGIOSTATIN FILE REFERENCE: 032303-005
CURRENT APPLICATION NUMBER: US/09/086,514
CURRENT FILING DATE: 1998-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SUZUKI, Kazuyasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: JP 317250/1996
EARLIER FILING DATE: 1996-11-28
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL LOCATION: (1)..(19)
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                       Local Similarity 31.8 nes 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 MVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 FDCGKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 FPCGRPWKRMEKKRSHLKRDTEDQEDQVDP-----RLIDGKMTRRGDSPWQVVLLDSKKK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 RAGLEKNYCR---
  565 FDCGKP--
                                          139 FPCGRPWKRMEKKRSHLKRDTEDQEDQVDP----RLIDGKMTRRGDSPWQVVLLDSKKK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 RSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGD--DLLQCHPAVK 138
                                                                                                                                       81 RSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGD--DLLQCHPAVK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSTTUNDIALLHLAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWGYHSSREK 308
                                                                                               RAGLEKNYCR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGP 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAKRNRTFVLNFIK---IPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TRKDIALLKLSSPAVITDKVIPACLPSPNYVVADR-----TECFITGWG-
                                                                                                                                                                                    17.6%; Score 410; DB 3; Length 810; 31.8%; Pred. No. 9.3e-27; ative 47; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NPDGDVGG
                                                                                               ---NPDGDVGG----
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---QVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRFGM 604
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                                                                                               ---PW--CYTTNPRKLYDYCDVPQC-AAPS 564
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Papkoff, Jackie
APPLICANT: Megabios Corporation
APPLICANT: Megabios Corporation
APPLICANT: Megabios Corporation
APPLICANT: Megabios Corporation
APPLICANT: Megabios Corporation
FITTLE OF INVENTION: Inhibition of Angiogenesis by Delivery of Mucleic Acids
FILE EXPERENCE: 018484-000110US
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US-09-192-012-5
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Patent No. 6475784
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 LACGAVLIHPSWYLTAAHCMDESKK----LLYRLGEYDLRRWEKWELDLDIKEVFYHPNYS 250
764 LVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRN 809
                                                                                           364 MVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD 409
                                                                                                                                                                                  706 --ETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGP
                                                                                                                                                                                                                                                       309 EAKRNRTFVLNFIK---IPVVPHNECS--EVMSNMVSENMLCAGILGDRQDACEGDSGGP 363
                                                                                                                                                                                                                                                                                                                                                   662 ---TRKDIALLKISSPAVITDKVIPACLPSPNYVVADR----TECFITGWG---
                                                                                                                                                                                                                                                                                                                                                                                                                                          251 KSTTDNDIALLHLAQPATLSQTIVPICLPDSG--LAERELNQAGQETLVTGWGYHSSREK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523 RAGLEKNYCR-----NPDGDVGG-----PW--CYTTNPRKLYDYCDVPQC-AAPS 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 RSGWEGRFCOREVSELNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGD--DLLQCHPAVK 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.6%; Score 410; DB 4; Length 810; 31.8%; Pred. No. 9.3e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
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RESULT 147 US-09-403-736-1

Sequence 1, Application US/09403736

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                                                                                                                                                                                                                                                   ;Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
;PATRICK J.;PINGEL, KURT;YOSHTAKE, SHINJI
                           ;SEQ ID NO:8:
                                                                                                                                                                                           ;ACTIVATORS
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PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/044,980
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: A2778A-US
CURRENT APPLICATION NUMBER: US/09/403,736
CURRENT FILING DATE: 1999-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Adenovirus-Mediated Intratumoral Delivery Of An Angiogenesis Anta
TITLE OF INVENTION: For The Treatment of Tumors
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ORGANISM: humanplasminogen
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                                                           NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 22-MAY-1987
                                                                                                                                                                                                                           TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hes 110;
LENGTH: 810
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OPOLON, Paule
SORIA, Claudine
RAGOT, Thierry
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SORIA, Jeanette
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                                                                                             US/07/53,412
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Patent No. 5952431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 110; Conservative 47; Mismatches 113; Indels
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Best Local Similarity 31.8%;
                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 267 amino active active services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second services of the second service
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
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   STRANDEDNESS:
                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                  NAME: Plumer, Elizabeth R
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                               amino acid
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                                                              267 amino acids
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; MOLECULE TYPE: No. 5968782e US-08-978-404B-18
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Best Local Similarity
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APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
RELEPHONE: 617-720-3500
TELEPHONE: 617-720-3500
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stevens, Richard L.
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Search completed: June 14, 2004, 17:48:59 Job time : 34 secs

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Homo sapiens

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Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulatio sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antiangin anticoagulant; therapy.	¥i.	15	ΑA	RESULT 1 AAB82673 ID AAB XX																								115	114	112	111	109	108	106	104	103	101	99 100
	Wild-type human protein C.	-0CT-200	AAB82673;	82673		1407 1406	1409	2085	2244 2210	2257.5	2281 2270	2286	2290 2288	2294	2295.5	2298	2302 2298	2304.5	2307	2308	2308	2309 2309	2309	2310	2310	2310	2311	2311	2311	2311	2311	2312	2312	2312	2312 2312	2312	2313	2313 2313
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oagulation; stenosis; antianginal						Human	Human	PAP-	Hybrid		Human		Human		Human		Human pro	Human		Human		Human Human		Human	Human	Human	Human		Human		Human		Human Human	Human	Human	Human	Human	Human Human
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                                  Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
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                                                                                                                                                                                                                                                                                            /156...157
/mote= "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
158...169
/note= "activation peptide; removal activates the 2-chain zymogen"
159...170
/note= "thrombin cleavage site"
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141. .277
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The present sequence is that of human protein C mature polypeptide. The

Claim 1; Page 49-50; 63pp; English.

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RESULT 2
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CC transformed host cells and a method of producing the human protein C derivatives and disease states predisposing to thrombosis (e.g. myocardial CC typercability increasing protein or with tissue factor pattway inhibitor), CC comparished thrombotic occlusion, thrombosis in protein C deficiency, caute arterial thrombotic occlusion, thromboshism, or stenosis in C coronary, cerebral or peripheral arteries or in vascular grafts. Human CC patients with genetically predisposed prothrombotic disorders may be treated by grafts there we will laimed!
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 419 AA;
                     protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic d myocardial infarction; angina; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treated by gene therapy (all claimed)
                                                                                                           Human protein C derivative 1.
                                                                                                                                                          26-FBB-2001
                                                                                                                                                                                                                                              AAB36894 standard; protein; 419 AA
                                                                                                                                                                                                       AAB36894;
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                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              increased resistance to inactivation by serpins when compared to wild-
type activated human protein C. They also have longer half-lives in human
blood and hence require either less frequent administration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predisposing thrombosis, comprises specific amino acid substitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           smaller dosage than wild type human protein C for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 42-44; 57pp; English
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWBKWELDLDI
                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                             GYHGSREKEAKENRTIFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                    KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQBTLVTGW 300
                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                     GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQBTLVTGW
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Pred. No. 3e-143;
0; Mismatches 0
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Gaps

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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP

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300

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                                                                                                                           Matches 419;
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mature wild type protein C.
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                                                                                                                                                                                                                                                protein; thrombotic arterial thrombotic occlusion, protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present segmence is human mature wild type protein C
                                                                                                                                                                                                                                                                                                                                                                           unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sikle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-2000; 2000US-0181948P.
14-MAR-2000; 2000US-0189199P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substitutions at specified amino acid positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein {\mathbb C} derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thromboembolism; prothrombotic disorder; gene therapy; thalassaemia
                                                                                                                                                                                                            Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of acute coronary syndromes e.g. myocardial infarction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO ELI.
    61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                          1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                         ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                           Conservative
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                                                                                                                                                 Pred. No. 3e-143;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU99002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99002 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Protein C zymogen protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2002
                                                                                                                                                            18-OCT-2000;
18-OCT-2000;
                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                         Peptide
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                        N-PSDB; ABK86039
                                                                 Andersen KV,
                                                                                                                                                 21-JUN-2001;
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                                        2002-489875/52.
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                                                                                            MAXYGEN APS.

MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVFVHENYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW 300
                                                                                                                                  ; 2000DK-00001560.
; 2000US-0242268P.
; 2001DK-0000970.
; 2001US-0300154P.
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                                                                                                                                                                                                       2001WO-DK000679
                                                                  Pedersen
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                         /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                              /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                 /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                        /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 419 AA
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                                                                 Freskgaard PO;
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Novel conjugate useful for treating or preventing septic shock, stroke

attached to protein C polypeptide comprising an attachment group. and myocardial infarction, comprises non-polypeptide group covalently

Claim 2; Page 79-81; 92pp; English.

diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced repail clearance. attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the provise that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Arm/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/naveravian) of strate and interaction after variance (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents zymogen increased serum half-life, increased resistant to inhibitors, reduced remain clearance, reduced immunogenicity and/or increased bloavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammaatory activity of APC bleeding while maintaining the antiinflammaatory activity of APC polypeptide moiety (II) The invention relates to a conjugate (I) comprising at least one nonprotein C upon which the variants of the invention were based introduced and/or at least one removed amino acid residue comprising an olypeptide moiety (II) (e.g. an N-glycosyl group) covalently atta protein C polypeptide comprising an amino acid sequence which di rom that of a parent protein C polypeptide (III) in at least one covalently attached to differs

Sequence 419 AA;

Matches 419; Query Match Local similarity Conservative 100.0%; 0 Score 2324; DB 5; Pred. No. 3e-143; Mismatches 0 Indels Length 419; 0 Gaps 0

밁 Ş 밁 5 밁 8 밁 Ş 뮍 8 몂 S 361 301 121 121 301 241 241 181 181 61 61 ப GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS SPWQVVILLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300 300 240 180

THE X SO XXW WX XX DX XC ABR55547; antithrombotic; antiinflammatory; antiapoptotic; profibrinolytic; hypercoagulative disease; thrombosis; myocardial infarction; pulmonary embolism; reocclusion; angioplasty; thrombomodulin. 11-AUG-2003 ABR55547 Protein C; coagulation; thrombin; fibrinopeptide A; serine protease; Amino acid sequence of mature human protein C (PC) 19-OCT-2001; 2001FR-00013492 19-OCT-2001; 2001FR-00013492 25-APR-2003 FR2831170-A1 Region Active-site Homo sapiens Aiach M; Le Bonnec B, Marque PE, (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. Region standard; (first /note= "heavy chain" /note= "light chain" Location/Qualifiers protein; 419 entry) Louvain V, ΑA Calmel C, Bianchini E;

New chimeric protein, cleavable by thrombin, useful e.g. as antithrombotic agents, particularly modified protein C containing Disclosure; Fig 1; 51pp; French. artificial activation sequence.

WPI; 2003-451127/43.

The present sequence represents the mature form of human protein C. This protein is an essential factor in the regulation of coagulation. The specification describes a chimeric protein, based on protein C, which comprises a thrombin-cleavable artificial sequence. This artificial sequence is of a formula given in the specification, and comprises a peptide from fibrinopeptide A, and a thrombin-cleavage site, other than that of the alpha-chain of fibrinogen. The chimeric protein and serine hypercoagulative diseases, e.g. venous and arterial thrombosis; myocardial infarction; pulmonary embolism; reocclusion after angioplasty and alterations in the genes for protein C and thrombomodulin protease derivatives obtained by cleaving the chimeric protein with thrombin, are useful as antithrombotic, antiinflammatory, antiapopto and profibrinolytic agents, for treatment or prevention of antiapoptotic

Sequence 419 AA;

뮹 S Query Match Best Local 9 419; Similarity ANSFLEELRHSSLERECIEEICDFSEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 Conservative 100.0%; Score 2324; DB 6 100.0%; Pred No. 3e-143; 0 Mismatches 6; 0 Indels Length 419; 0 60

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SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC40014 standard; protein;
                                                                                                                                                                                                             Pharmaceutical composition comprising activated protein C and a chelating agent useful for treating thrombotic disorders such as stroke, deep vein thrombosis, pulmonary embolism and myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intravascular coagulation; thrombotic stroke; deep vein thrombosis; pulmonary embolism; peripheral arterial thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
                                                                                 thrombosis, pulmonary embolism, peripheral arterial thrombosis, acu myocardial infarction and retina thrombosis. The present amino acid
                                                                                                            The invention comprises a pharmaceutical composition containing activated protein C (aPC), a chelating agent and optionally a diluent. The composition of the invention is useful for treating thrombotic disorders, such as: intravascular coagulation, thrombotic stroke, deep vein
                                                                                                                                                                                                                                                                                                                                                               08-MAR-2002; 2002US-0363364P
                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003; 2003WO-US005046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                        Sequence
                                                    sequence represents a human protein that was used of the invention.
                                                                                                                                                                                   Disclosure; SEQ ID NO 3; 29pp; English.
                                                                                                                                                                                                                                                                          WPI; 2003-722308/68
                                                                                                                                                                                                                                                                                                     Gopalrathnam G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myocardial infarction; retina thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
16-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP81104 standard; protein; 460 AA.
                                       Sequence 460
                                                                 The human protein C is expressed in large amts. using plasmid pPC 1 E.coli K12/Om 225 (FERN P-9297). (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of human protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP81104;
                                                                                                                               Disclosure; Page ?; 16pp; Japanese
                                                                                                                                                         sequence.
                                                                                                                                                                        Human protein C gene - prepd. from new DNA having specified base
                                                                                                                                                                                                       N-PSDB; AAN81408
                                                                                                                                                                                                                     WPI; 1988-350711/49.
                                                                                                                                                                                                                                                                                                         21-APR-1987;
                                                                                                                                                                                                                                                                                                                                     31-0CT-1988.
                                                                                                                                                                                                                                                                                                                                                                  JP63263083-A.
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SICCGHGTCIDGIGSFSCDCRSGWEGRFCQRBVSFINCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                              87JP-00096341
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                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid pPC
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100.
 Score 2324; DB 1;
Pred. No. 3.3e-143;
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Query Match

100.0%;

Score 2324;

DΒ 7;

Length 419;

Query Match
Best Local Similarity

. 04 ,

Length

B H

Matches

Length Indels

461; 0

Gaps

102

60

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Vascular disorder therapy; protein C deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of polypeptide with human protein C activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
25-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP60001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP60001 standard; protein;
                                                                                                                WPI; 1986-220077/34.
                                                                                                                                                 Santerre RF;
                                                                                                                                                                                                                               08-FEB-1985;
                                                                                                                                                                                                                                                              06-FEB-1986;
                                                                                                                                                                                                                                                                                                20-AUG-1986
                                                                                                                                                                                                                                                                                                                               EP191606-A.
The claimed sequence AAN60001 has "RIN-RM"
                                Disclosure; Page 10-12; 121pp; English.
                                                                                                                                                                                             (ELIL ) LILLY & CO ELI.
                                                           in. of polypeptide having human protein C activity - is by recombinant
procedures for prod. useful against vascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVÅSFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDMIHGHIRDKEÅPQKSWAP 419
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                                                                                                                                                              Beckmann RJ,
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(first entry)
                                                                                                                                                                                                                               85US-00699967
                                                                                                                                                                                                                                                              86EP-00300823
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                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Best Local :
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 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                Human Protein
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10-MAY-1991
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                                                                                 Disulfide-bond Modified-site
                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                human Protein C; anti-coagulant; thrombosis; serine protease
                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 100.0%; Score 2324; DB 1; al Similarity 100.0%; Pred. No. 3.3e-143; 419; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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   /label= N-glycosylation site
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1 147. .160
1 162. .175
1 183. .319
                                                                                                                                                                                                                            59. .64
                                                                                                                  101. .106
105. .120
                                                                                                                                                                                                                                                /label= prepro leader peptide
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                /label= gamma-carboxyglutamic acid
                                                                                                                                                                /label= growth
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murray MJ, Berkner KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1985;
15-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26~JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinantly produced protein C can be used to treat thrombotic disorders such as venous thrombosis as it has anti-coagulant properties. The protein sequence is thought to yield two peptide chains; the first contains the Gla domain and growth factor domains and the second (the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activation peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 4; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein \mathbb C or activated protein \mathbb C - prepd. using expression vector capable of integration in mammalian host cell DNA.
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                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                           ANS FLEELRHSSLERECIEEICD FEEAKEIF QUVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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85US-00766109
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197. .198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "in heavy chain; converts to activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "apparent processing site for connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "apparent processing site for connecting dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= N-glycosylation site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contains the catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2324;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 461;
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RESULT 10
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                                                            believed to be removed (on basis of homology with bovine protein C), believed to be removed (on basis of homology with bovine protein C), cresidues 197-8 or 199-200), followed by carboxypeptidase or residues 197-8 or 199-200), followed by carboxypeptidase or caminopaptidase action, to form 2 chain protein C; residues 200-211 constitute the activation peptide, which is removed from the zymogen constitute the activated protein C; residues 212-461, once post cranslationally modified, constitute the activated heavy chain of active protein C; and the heavy chain of the 2 chain form of protein C zymogen, once post-translationally-modified, is composed of residues 200-461. Conce post-translationally-modified, is composed of residues 200-461. Conce post-translationally-modified, is composed of residues 200-461. Conce post-translationally-modified, is composed of residues 200-461. Conce post-translationally-modified protein C are regulators of haemostasis, composing from native protein C by increased sensitivity to activation by thrombin and thrombin/ thrombomodulin (even in presence of Ca ions) and confidence in vivo half life. They are useful as on-demand antithrombotic agents, (replacements for heparin and hydroxycoumarins) and for treatment confidence in the protein C deficiency states. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
01-NOV-1989
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                                                                                                                                                                                                                                                                                                                                                                                           This is the protein sequence of mascent human protein C encoded by the DNA of AAN90187, which is derived from cDNA clones prepd. from human liver mRNA. It comprises the following regions: residues 1-42 are the signal peptide and propeptide of human protein C, important for directing secretion and gamma-carboxylation of protein C; residues 43-197, once post- translationally modified, constitute the light chain of both the two-chain zymogen and activated forms of protein C; residues 198-9 are believed to be constituted forms of protein C; residues 198-9 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein C; zymogen form; activated C protein; human liver mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP90401 standard; protein; 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA encoding zymogen form of human protein C - and its activated deriv., useful as e.g. antithrombotic agents more sensitive to thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP323149-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal peptide; propeptide; antithrombotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zymogen form of human protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 4 - 7; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activation.
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(first entry)
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agents, (replacements to Triency states. of hereditary protein C deficiency states. correct PA field.)

Sequence 461 AA

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RESULT 11
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                                                  ZYMOGENETICS INC
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miyagi F,
                                                                                                                                                                                                                                                             25-MAR-2003
30-SEP-1991
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                                                                                                                                           gla-domain; VKDP
                                                                                                                                                                                                               Human protein C.
                                                                                                                                                                                                                                                                                                                                  AAR13081;
                                                                                                                                                                                                                                                                                                                                                                              AAR13081 standard;
                            Peptide
                                                                                                Homo sapiens
                                                                                                                                                            Phopholipid; binding protein; lipocortin; domain; vitamin K; PBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                  Location/Qualifiers
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Pred. No. 3.3e-143;
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                                                                          RESULT 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence, or a fragment of it, is used in the construction of hybrid phospholipid-binding proteins (PBP) having the same biological activity as human protein C or human activated protein C. The hybrid sequence would comprise at least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-I, joined to a gla-domainless protein C or activated protein C. See AAQ12680-81 for such examples. See also AAQ12678-81. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant prodn. of hybrid phospholipid-binding proteins - comprising lipocortin phospholipid-binding domain and vitamin=K-dependent protein.
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 25-MAR-2003
                        AAR13074;
                                                AAR13074 standard;
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                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                                                                                                                                                        APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                              GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                   GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNWVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                          SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                 GYHSSREKEAKRINRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                             KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERBLNQAGQETLVTGW
                                                                                                                                                                                                                                                                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCNDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 461
                                                                                                                                                                                                                      KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
(revised)
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/label= mat_protein
                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2324; DB 2;
100.0%; Pred. No. 3.3e-143;
tive 0; Mismatches 0;
                                                   461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C precursor
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  The sequence was deduced from a clone isolated from a cDNA library prepd. from mRNA from Hep G2 cells. It is a protein C precursor, including light
                                        Disclosure; Fig 1; 60pp;
                                                                                                                                               Foster DC,
                                                                                                                      1991-222903/30.
                                                                                                                                                                        ZYMOGENETICS INC
TEIJIN LTD.
                                                                                                         AAQ12649
                                                                                                                                               Holly RD,
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                                         English.
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S 멿 8 뭉 Š 붕

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Recombinant protein C with truncated light chain anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= N-glycosylation site
197. .198
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43. .79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= pre-pro peptide
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                                                                                                                                                                                                                                                                                                                                            /label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= proteolytic cleavage 99. .200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= gamma carboxyglutamic
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc and heavy chains, which is cleaved to produce activated protein C (see feature table). The DNA encoding the sequence can be manipulated by comparising techniques to express a protein comprising (when extivated) a heavy chain and a truncated light chain comprising residues to comprise the precursor of formula: Pre-pro-L-X-H Pre-pro = pre-pro comprises the precursor of formula: Pre-pro-L-X-H Pre-pro = pre-pro comprises the precursor of formula: Pre-pro-L-X-H Pre-pro = pre-pro comprises the precursor of formula: Pre-pro-L-X-H Pre-pro = pre-pro comprises the protein C with all/part replaced by the corresponding peptide of either protein S, factors VI, IX or X, or prothrombin; L = AAS 1-149, comprises the protein S, factors VI, IX or X, or prothrombin; L = AAS 1-149, comprise the protein S, factors VI, IX or X, or prothrombin; L = AAS 1-149, comprise the protein S, factors C, and C, and H = heavy C (bahin. Cells transformed with expression vectors conts. the modified DNA compression vectors conts. the modified DNA compression to the protein S, factors C (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                          protein C; heavy chain; light chain; anticlotting; fibrinolysis;
promoter; anticoagulant.
                                                                                                                                                                                                                                                            Protein C.
                                                                                                                                                                                                                                                                                                 10-AUG-1993
                                                                                                                                                                                                                                                                                                                                    AAR34295;
                                                                                                                                                                                                                                                                                                                                                                 AAR34295 standard; protein; 461
                Peptide
                                                                  Peptide
                                                                                                                                                                         Homo sapiens
                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGYKLGDDLLQCHBAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPMVASFHGTWFLVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWBLDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPMVASFHGTWFLVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKBAPQKSWAP 461
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                /note= "light chain"
200. .211
                                                   /label= C-terminal
   /label= N-terminal
                                                                                                       'labe1= C-terminal
                                                                                                                                    ocation/Qualifiers
                                                                                    "light chain"
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Matches 419; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein C and activated protein C with short H chains - useful as anti-clotting agents and fibrinolysis promoters.
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                                                                                                                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHDSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SICCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFIEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDGEDQVDPRLIDGKWTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSPLEELRHSSLERECIBEICOFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVKLGEYDLRKWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                            GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                        GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
ĠĠ₽ŃVASŦĦĠŢWŦĹVĠĹVŚWĠEĠĊĠĹĹĦŊYĠVŸŢĸVŚŔŶĹŊWĬĦĠĦĬŔŊĸŒĂPQĸŚWAP
                                                                                                                                                                                                                      KEVFVHRINSKSTTDNDIALLHLAQPATISQTIVAICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91JP-00228687
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451. .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2324; DB 2; 100.0%; Pred. No. 3.3e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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419 461

402

300 282

AAW02600 standard; protein; 461 AA

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25-MAR-2003
05-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activated protein C; serine protease; thrombosis; thrombolytic; fibrinolytic; antithrombotic; blood clotting; therapy.
                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                              Cleavage-site
                                                                                                                                                                                                             Misc-difference
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          Disulfide-bond
                             Disulfide-bond
                                               Cleavage-site
                                                                              Misc-difference
                                                                                                                                                             Misc-difference
                                                                                                                                                                                Cleavage-site
                                                                                                  Peptide
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(first entry)
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105
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                                                                                                                                                                                                               196
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                                                                                                                                       /note= "residues 198-199 are replaced by Lys-Lys or Arg-
Arg in constructs of the invention"
                                                                                                                                                                                  197. .198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Pre-pro-peptide
                                                                                                          activation peptide"
                                                                                                                                                                                         constructs of
                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "forms disulphide bond with Cys106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "forms disulphide bond with Cys101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "forms disulphide bond with Cys111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= GLA_domain
                                                        /note= "residue 200 is replaced by Ala, Ser,
in constructs of the invention"
                                                                                                                                                                                          /note= "residue 196 is replaced by Lys, Arg or in
constructs of the invention"
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                                                                                                                                                                                                                                                                                                                                                                                                         note= "forms disulphide bond with
/note= "forms disulphide bond with Cys238"
                                                                                                                    note= "cleavage site between connecting dipeptide
                                                                                                                                                                      note= "cleavage site for connecting dipeptide"
                                                                                                                                                                                                                                           note= "forms disulphide bond with Cys162"
                                                                                                                                                                                                                                                                                                                                                                   label=
                   note= "forms disulphide bond with Cys254"
                                     note= "cleavage site for activation peptide
                                                                                      label= Activated_protein-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 "forms disulphide bond with Cys92"
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                                                                                                                                                                                                                                                              disuphide bond with Cys175"
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                                                                                                                                                                                                                                                                                                                          disulphide bond with Cys160"
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                                                                                                                                           Matches 419;
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29-OCT-1986;
08-DEC-1987;
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                                                                                                                                                                                                                                                                                                                                  New DNA encoding modified forms of opt, activated protein {\tt C} - and related transformed cells for prodn. of recombinant protein C for use e.g. as an anti-thrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                            Murray MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1996.
                                                                                                                                                                                  Sequence 461 AA;
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(ZYMO ) ZYMOGENETICS INC
Berkner KL,
                                                                    86US-00924462.
87US-00130370.
89US-00317205.
90US-00582131.
92US-00987532.
                                                                                                                                                                     85US-00749600
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                                                                                                                                                                                                                                                                                                                                    /note= "forms disulphide bond with Cys426" 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= N-glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                 "forms disulphide bond with Cys387"
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                                                                                                                                                                                                                                                                                                                    "forms disulphide bond with Cys 398"
                                                                                                                                                                                                                                                                                                                                                                                           "forms disulphide bond with
   Foster
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Example 1; Fig 2A-C; 34pp; English.

Human protein C (AAW02600) is a zymogen of a serine protease that plays an important role in the regulation of blood coagulation and the generation of fibrinolytic activity in vivo. It is synthesised in the liver and processed to a 2-chain molecule, which is itself converted to activated protein C. Protein C and activated protein C are useful in the treatment of thrombotic disorders. They can be produced e.g. in mammalia host cells using a cDNA clone (AAT32795) derived from Hep G2 cells. Variant protein C, modified to improve cleavage between the heavy and light chains of the circulating intermediate, can also be produced. (Updated on 25-WAR-2003 to correct PF field.) in mammalian

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103 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                      61 SLCCGHGTCIDGIGSFSCDCRSGMEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                           1 ANSFLEETRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                APGYKLGDDLLQCHPAYKFPCGRPWKRMEKKRSHLKRDTBDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                            ANSFLEBLRHSSLERECIEEICDFBEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                  Score 2324; DB 2;
Pred. No. 3.3e-143;
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                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                    Gaps
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Length 461;

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RESULT 16
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В
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                                                                               Matches
                                                                                                                 Query Match
                                                                                                                                                                                                                 AAZ32159 to AAZ32194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic analysis. AAY49550 to AAY49573 represent the proteins which correspond to some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                medicine; genetic analysis; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; coding sequence polymorphism; vascular pathology gene; polymorphic site; phenotype correlation; forensic; paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lecithin cholesterol acyltransferase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY49561 standard; protein; 461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of polymorphisms in genes, predisposition to vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 24; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                         Sequence 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                                                                                                  Local
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                       ANSFLESCRHSSLERECIBEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
ANSFLEELRHSSLERECIBEICDFERAKEIFONVDDTLAFWSKHVDGDQCLVLFLEHPCA 102
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ilarity 100.0%;
Conservative C
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                                                                          Score 2324;
Pred. No. 3.3
0; Mismatches
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ches 0;
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SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                  GGPMVASEHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; sepsis; protein C deficiency; occlusion; thromboembolism; attenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal;
                                                                                                                                                                                                                                                                               Wild-type human protein C.
                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2001
anticoagulant; therapy.
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Homo sapiens

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Disulfide-bond
Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide
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                                                                                                                                                                                                                                                           /note= "0-phosphorylated"
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resistance to inactivation by sexpins compared with wild-type human protein C but retain the biological activity of the wild-type protein. The amino acid substitutions are selected from HIO, SIIG, SIZK, Q32K, CM 33D, N33F, and amino acids at positions 194, 195, 228, 249, 254, 302, or 316 of the mature protein C polypeptide substituted with Ser, Ala, Thr, CM His, Iys, Leu, Arg, Asn, Asp, Glu, Gly or Gln (numbering relative to the protein C mature protein sequence). Preferred protein C derivatives are protein C derivatives are a vector comprising NNA encoding the novel human protein C derivatives, transformed host cells and a combination with bactericidal permeability increasing protein C derivatives are useful for treating coronary syndromes and disease states compared to thrombosis (e.g. myocardial infarction and unstable comparison), vascular occlustive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with hartering that the combosity of the protein of the protein or with the protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein or with protein 
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Disulfide-bond
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14-MAR-2000; 2000US-0189197P.
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                                                tissue factor pathway inhibitor), Ehrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral atteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to human protein C derivatives having at least 2 amino acid substitutions, and to recombinant DNA molecules encoding such derivatives. These derivatives have increased anticoagulant activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein C derivative for treating, e.g., myocardial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of human protein C prepro-polypeptide. The
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Query Match

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Score 2324;

멂 4:

Length 461;

Sequence 461 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic disorders; myocardial infarction; angina; stroke.
The present invention relates to a human protein C derivative. The protein is useful for treating vascular occlusive disorders, hypercoagulable states such as sepsis, disseminated intravascular coagulation, purpura fulminans, major trauma, major surgery, burns, adult
                                                                                                                   protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states predisposing thrombosis, comprises specific amino acid substitutions.
                                                                                                                                                                                  N-PSDB; AAC83312.
                                                                                                                                                                                                                                  Gerlitz BE, Jones BE;
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                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein C derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB3 6895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36895 standard; protein; 461 AA
                                                                                    Claim 1; Page 44-46; 57pp; English.
                                                                                                                                                                                                   WPI; 2001-007227/01.
                                                                                                                                                                                                                                                                                                  30-APR-1999;
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                                                                                                                 predisposing thrombosis, comprises specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKBAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNWVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLIQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APGYKLGDDLLQCHPAVKFPCGREWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
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Best Local
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type activated human protein C. They also have longer half-lives in human
blood and hence require either less frequent administration and/or
smaller dosage than wild type human protein C for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uremic syndrome, and also useful for treating thrombotic disorders and acute coronary syndromes such as myocardial infarction, unstable angina, and stroke. Protein C derivatives with amino acid substitutions result in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     respiratory distress syndrome, transplantation, deep vein thrombosis, heparin-induced thrombocytopenia, sickle cell disease, thalassemia, v hemorrhagic fever, thrombotic thrombocytopenic purpura, and hemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human wild type protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                     haemolytic uremic syndrome; acute arterial thrombotic occlusion;
thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
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                                                                                                                                                          /label= Signal_peptide
                                                                        /label= Mature_human_wild type_protein_C
                                                                                                                                                                                                                                               Location/Qualifiers
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Pred. No. 3.3e-143;
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WO200159084-A1

361 GGPMVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human wild type protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein, thrombotic disorders in combination with an anti-platelet agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. mycoardial infarction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-2000; 2000US-0181948P.
14-MAR-2000; 2000US-0189199P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-2001; 2001WO-US001221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 44-46; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA
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                                                                                                                                                                                                                                                                                                                                                          SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                    GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWBLDLDI
                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                       APGYXLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                              SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                               ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 102
GYHSSREKBAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 402
                                                                               KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
                                                                                                                 KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                APGYKLGDDLLQCHPAVKPPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grinnell BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2324;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3e-143;
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403

GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP

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The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached t a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245cs/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr3025er/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sepsis; septic shock; embolism; pulmonary embolism; burn; bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-1 antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU99001 standard; protein; 461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000; 2000DX-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DX-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                          Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                               Example 4; Page 76-77; 92pp; English.
                                                                                                                                                                                                                                                                                                              N-PSDB; ABK86038.
                                                                                                                                                                                                                                                                                                                             WPI; 2002-489875/52.
                                                                                                                                                                                                                                                                                                                                                            Andersen KV, Pedersen AH,
                                                                                                                                                                                                                                                                                                                                                                                           (MAXY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Protein C; N-glycosylation; APC; activated protein C; prechalf-life; chromosome 2q13-q14; stroke; myocardial infarctivenous thrombosis; disseminated intravascular coagulation;
                                                                                                                                                                                                                                                                                                                                                                                           MAXYGEN APS.
MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Mature_protein_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                             Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pregnancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor,
                                                                                                                                                                     attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIC;
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88888888888888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
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  403
                                    361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ANSFLEELRHSSLERECIEEICDFEEAKEIPQNVDDTLAFWSKHVDGDQCLVLPLEHICA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on chromosome 2q13-q14. The present sequence represents procursor
                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACECDS
                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRECQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANSPLEELRHSSLERECIEEICDFEEAKBIPONVDDTLAFWSKHVDGDQCLVLFLEHECA 102
                                                                                                                                                                                    KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQETLVIGW
                                                                                                                                                                                                                                KEVEVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                              SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                               GYHSSREKEAKRINRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTREGD
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 2324; DB 5; 100.0%; Pred. No. 3.3e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gars
                 461
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AAU99035 standard; protein; 419
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23-AUG-2002

(first entry)

Human Protein C zymogen protein mutant S252N

RESULT 21
AAU99035
ID AAU99037
XX AAU99037
AC AU990
XX AAU990
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2ql3-ql4; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;

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CC polypeptide moiety [II] (e.g. an N-glycosyl group) covalently attached to golypeptide moiety [II] (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide (III) in at least one comprising an amino acid sequence which differs comprosed and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation could residue comprising an constitution in a position (P) where (P) is an amino acid with at least consubstitution in a position (P) where (P) is an amino acid with at the group exposed to the surface, with the proviso that the gravitation is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, [II] comprising a substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, [IV] (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (M2) the functional in vivo half-comprising (V) or (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (S) interessing (VI); (
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18-OCT-2000; 2000US-0242268P.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200232461-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAXY-) MAXYGEN APS
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while maintaining the antiinflammatory activity of APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pedersen AH, Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= Heavy_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eı= Lys_Arg_dipeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The presents sequence represents a zymoger protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 419 AA;
                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                       121 APGYKLGDDILQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                    301
                                                                                                                          301
                                                                                                                                                                    241
                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                        181
  361
                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSLDWGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANSFLEETRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVFHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                    KEVFVHPNYSKNTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                  GYHSSREKEAKKNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%;
99.8%;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2321; DB 5;
Pred. No. 4.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a zymogen
                                                                                                                                                                             300
                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                         240
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RESULT 22
                                                                                                                                                                                               Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; prequancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-l antitrypsin; mutant; mut
                                                                                                                 Key
Protein
                                                                                                                                                                                                                                                                                         Human Protein C zymogen protein mutant S250N
                                                                                                                                                                                                                                                                                                                                                                          AAU99031 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                      23-AUG-2002
                                                                Protein
                                                                                        Peptide
                                                                                                                                                          Synthetic
                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                158 . . 419
                                                                                                      /label= Light_chain
                                                                                                                               Location/Qualifiers
                                                  /label=
                                                                             /label=
                          label= Activation_peptide
                                                                                           .157
                                          . 169
                                                  Heavy_chain
                                                                           Lys_Arg_dipeptide
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Misc-difference 250

/note= "Wild-type Ser substituted by Asn"

W0200232461-A2.

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                                                                                                                                                                                                                                                                       changes is prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow (C transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 (C increased resistance to activation by e.g. human plasma and alpha-1 (C increased serum half-life, increased in vivo half-life, increased increased in two half-life, increased increased in the carried complete offers a number of advantages over the currently available (C renal clearance, reduced immunogenicity and/or increased bloavailability. (C renal clearance, including longer duration between injections, available (C APC products, including longer duration between injections, cardinal stration of less protein, and fewer side effects. Moreover, a creduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                            Matches
                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000;
18-OCT-2000;
21-JUN-2001;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claım 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-0CT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                          located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substitution
                                                                                                                                                           Sequence 419
                                                                              418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAXYGEN HOLDINGS LTD
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                                      ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
ANSFLEEURHSSLERECIEEICDFEBAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000DK-00001560.
; 2000US-0242268P.
; 2001DK-00000970.
; 2001US-0300154P.
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                                                                              Conservative
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                                                                                                 99.9%;
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    Mismatches

                                                                                                 Score 2321; DB 5;
Pred. No. 4.8e-143;
                                                                                                                      멂
                                                                                                                    5;
                                                                                                                  Length 419;
                                                                                Indels
                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding cell (VII)
                                                                                Gaps
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RESULT 23
AAP81205
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This protein C sequence is obtd. upon transformation of mammalian host cells with a recombinant DNA sequence comprising cDNA and genomic DNA (minus introns) encoding protein C. The prod. collect- ed upon culturing of the cells has substantially the same biologic- al activity as natural protein C and is hence useful in the treat- ment of blood coagulation

Protein C DNA coding sequence and expression vector for prodn. - used for

blood coagulation disorders

Page ?; 35pp;

English

N-PSDB; AAN81563, AAN81564

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43. .197
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                                                                                                                                                                                                                                                                                                                                                                          /note= "light chain"
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Pred. No. 5.2e-143;
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Matches Query Match

418;

Conservative

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Local

Similarity

99.98;

Score 2321; DB 1; Pred. No. 5.2e-143; Mismatches

Length 461; Indels

Sequence 461

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Nascent human protein C produces inactive protein C. It is used as an anti-coagulant in myocardial infarction and deep vein thrombosis. The patent discloses a recombinant way of making activated protein C. Amino acids 1-42 encode the signal peptide and propeptide, 43-197 constitute the light chain of both the zymogen and activated forms; 198-199 residues are believed to be removed to form 2-chain protein C; 200-211 are the activation peptides removed from the zymogen to form activated protein C; 212-461 constitute the activated heavy chain after post-translational modification. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                   GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSUMVSENMLCAGILGDRQDACEGDS
                                                                                             GYHSSREKEAKRURTFVLNEIKTPVVDHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDQSKKLLVRLGEYDLRRWEKWELDLDI 282
GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVÝTKVSRYLDWIHGHIRDKEAPQKSWAP
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KW Jones
KW adult
                                                                                 Human Protein C zymogen protein mutant V339T.
                                                                                                                                                           AAU99074 standard; protein; 419 AA
                                                                                                                                     AAU99074;
                                                                                                             23-AUG-2002
                                                                                                             (first entry
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sepsis; septic shock; embolism; pulmonary embolism; burn; bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-1 antitrypsin; Human, Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; pregnancy;
coagulant;
mutant; mutein.

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The invention relates to a conjugate (I) comprising at least one non-cc polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to Cc a protein C polypeptide comprising an amino acid sequence which differs cfrom that of a parent protein C polypeptide (III) in at least one set one can be attachment group for the mon-polypeptide group (e.g. an N-glycosylation catid stein Also included are (I) a variant (IV) of (III) comprising an constitution in a position (P) where (P) is an amino acid with at least consubstitution is not Thr2435er/Ala/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln comprising (IV); (3) an expression vector (VI) comprising (VI); (3) an expression vector (VI); (3) an uncleotide sequence (V) encoding (IV); (3) an expression vector (VI); (3) an expression (VI); (4) a host cell (VII) (CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-comprising (V) or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thromosis, distress syndrome (ARDS). The variant protein (DIC), sepsis, septic conjugates, variants and protein C parent protein (DIC), sepsis, septic conjugates variance, bare an increased in vivo half-life, increased resistant protein C has an conjugate syndrome (ARDS). The variant protein C has an conjugate syndrome (ARDS). The variant protein C has an conjugate syndrome (ARDS). The variant protein C has an conjugate syndrome (ARDS). The variant protein C has an conjugate syndrome (ARDS) and the conjugate syndrome conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in the conjugate syndrome conjugates have an increased in the conjugate syndrome conjugates have an increased in the conjugate syndrome conjugates have an increased in the conjugate syndrome
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18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-00T-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen KV, Pedersen
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(MAXY-) MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 419 AA;
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                                                                                                                                                                          KEVEVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEXDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKBMBKKRSHLKRDTBDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                         SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                             ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                   GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMTSENMLCAGILGDRQDACEGDS
                                                                                                                                            KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2320; DB 5;
Pred. No. 5.5e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 26
                                                                      Human Protein C zymogen protein mutant K251N.
                                                                            23-AUG-2002
                                                                                        AAU99033 standard;
                                                                             (first entry)
                                                                                        protein;
                                                                                         419
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Human, Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; adult respiratory is; septic shock; embolism; pulmonary embolism; burn; pregnancy; marrow transplantation; major surgery; trauma; ARDS; coagulant; distress syndrome; alpha-1 antitrypsin; mutant; mutein.

Homo sapiens.

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Synthetic.
            Misc-difference
                                                                                                                      Кeу
                                                          Protein
                                                                                 Peptide
                                                                                                         Protein
              251
                                                                                                                     Location/Qualifiers
                                      158.
/note= "Wild-type Lys substituted by Asn"
                                                                    /label=
                                                                                               /label= Light_chain
                         'label= Activation_peptide
                                                label=
                                                          91= Lys_Arg_dipeptide
,419
                                   .169
                                               Heavy_chain
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WO200232461-A2

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The invention relates to a conjugate (1) comprising at least one non-
CC polypeptide moiety (II) (e.g. an N-glycosy) group) covalently attached to
CC a protein C polypeptide comprising an amino acid sequence which differs
CC introduced and/or at least one removed amino acid residue comprising an
CC attachment group for the non-polypeptide (III) in at least one
CC site). Also included are (1) a variant (IV) of (III) comprising an
CC site). Also included are (1) a variant (IV) of (III) comprising a
CC substitution in a position (P) where (P) is an amino acid with at least
CC 54 of its side group exposed to the surface, with the proviso that the
CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII)
CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
CC life or the serum half-life of a parent protein C polypeptide. The
CC conjugates, variants and protein C proteins are useful as medicaments,
CC and in the manufacture of medicaments for the terestment (and
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                                                                       Вþ
                                                                                                                 8
                                                                                                                                                                       Matches
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, mycardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced remai clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-489875/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000; 2000DK-00001560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-2001; 2001WO-DK000679.
                                                                                                                                                                                                                                                                                                                                                                                                   APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000;
                                                                                                                                                                                                                                                                                                        located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                Sequence 419 AA;
                                                                                                                                                                                           Local
                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAXYGEN APS
                                                                                                                                                                                           Similarity
SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                          ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0242268P.
2001DK-00000970.
2001US-0300154P.
                                                                                                                                                                       Conservative
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                                                                                                                                                                                           99.8%;
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                                                                                                                                                                       0,
                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                    Score 2319;
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                                                                                                                                                                                              No.
                                                                                                                                                                                         6.4e-143;
                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                    Length 419;
                                                                                                                                                                       Indels
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                                                                                                                                                                     Gaps
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RESULT 27
AAU99125
AC AAU99
XX AU99
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XX Humar
XX Humar
XX Humar
XX Sprit
XX Sprit
XX Au99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU99015 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein C zymogen protein mutant D214N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU99015;
                                                                                                                                                                                                                                                 18-OCT-2000; 2000DK-00001560
18-OCT-2000; 2000US-0242268P
21-JUN-2001; 2001DK-00000970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-1 antitrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   after venous thrombosis, disseminance embolism; burn; pregnancy; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; sepsis; kRDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                             WPI; 2002-489875/52
                                                                                                                                                                                                                            21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001WO-DK000679
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                                                                                     Andersen
                                                                                                                                             (MAXY-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPMVASFHGTWELVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYHSSREKEAKDURTFYLNFIKIPVVPHNECSEVMSUMVSEUMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWBKWELDLDI
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                                                                                                                                             MAXYGEN HOLDINGS LTD
                                                                                                                                                                       MAXYGEN APS
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                                                                                                                                                                                                                               2001US-0300154P
                                                                                        Pedersen AH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Lys_Arg_dipeptide
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                                                                                        Freskgaard PO;
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CC introduced and/or at least one removed amino acid residue comprising an CC attachment group for the non-polypeptide group (e.g. an N-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising a CC substitution in a position (P) where (P) is an amino acid with at least CC syb of its side group exposed to the surface, with the proviso that the CC 53 of its side group exposed to the surface, with the proviso that the CC Tyr302ser/Ala/Thr/His/Iry/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) C comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC infe or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and C diagnosis/prevention) of stroke, myocardial infarction, after venous CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 c increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or intreased bioavailability. The conjugate offers a number of advantages over the currently available of Paper variant protein on the confidence included included increased resistant confidence in the confidence included included included included increased serum half-life, increased resistant to inhibitors, reduced the confidence included included included increased serum half-life increased serum half-life increased resistant to inhibitors.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide moiety (II) (e.g. an N-glycosyl group) covalently atta
a protein C polypeptide comprising an amino acid sequence which di
from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
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GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 6.4e-143;
                                                                                                                                                                         LLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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09-JAN-2003
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                                                                                                                                                                                                                             protein C Zymogen LIN comprises a signal peptide and propeptide of a gamma-carboxylated secreted protein, the light chain of HPC, a basic dipeptide (i.e. Lys-Arg, but can also be Arg-Lys, Lys-Gr Arg-Arg) and amino acid residues 200-461 of HPC but with Asp (214) replaced by Asn. The zymogen can be activated in vivo by thrombin alone (even in the presence of calcium) and is more susceptible to activation by thrombin/thrombomodulin than native HPC zymogen. Zymogen LIN can be thrombin/thrombomodulin than native HPC zymogen. Zymogen tin can be administered as a pro drug useful in prevention and treatment of diseases involving intravascular coagulation. It can also be given to thrombocytopenic patients with invasive cancers with effective and intensive chemotherapy. See ARR13537-40 and ARR13623. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPC mutant; pro drug; intravascular coagulation; zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein C zymogen LIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant mutants of human protein \mathcal C - having aminoacid changes increased sensitivity to activation by thrombin and thrombin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page 37-38; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-254444/35
                                                                                                                                                                                     Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombomodulin complex.
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                                                                                       1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
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                                                                                                                                          Similarity
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                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                             ANSPLEELRHSSLERECTEETCDFEEAKETFONVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                          Conservative
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198. .199
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Pred. No. 7.1e-143;
                                                                                                                             Mismatches
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The present invention relates to a human protein C derivative. The protein is useful for treating vascular occlusive disorders, CC hypercoagulable states such as sepsis, disseminated intravascular coagulation, purpura fulminans, major trauma, major surgery, burns, adult CC respiratory distress syndrome, transplantation, deep vein thrombosis, CC heparin-induced thrombostopenia, sickle cell disease, thalassemia, viral hemorrhagiz fever, thrombotic thrombosytopenia, sickle cell disease, and hemolytic CC uremic syndrome, and also useful for treating thrombotic disorders and acute coronary syndromes such as myocardial infarction, unstable angina, and stroke. Protein C derivatives with amino acid substitutions result in circeased resistance to inactivation by serpins when compared to wild-crype activated human protein C. They also have longer half-lives in human blood and hence require either less frequent administration and/or smaller dosage than wild type human protein C for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein C derivative 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states predisposing thrombosis, comprises specific amino acid substitutions.
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                                                                                                                                                                                                                                                                                           Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular cosquiation, DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mut
                                                                                                                                                                                                                                                                                                                                                                                           Human Protein C zymogen protein mutant V339S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU99073 standard; protein; 419
                                                                                                Misc-difference
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                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                         /label= Heavy_chain
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                                                                                                                                                                                                /label= Light_chain
                                                                                  'note= "Wild-type Val substituted by Ser"
                                                                                                              abel= Activation_peptide
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Pred. No. 7.5e-143;
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15-OCT-2001; 2001WO-DK000679

25-APR-2002

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CC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to copylopptide moiety (II) (e.g. an N-glycosyl group) covalently attached to compress of a protein C polypeptide (III) in at least one controduced and/or at least one removed amino acid sequence which differs controduced and/or at least one removed amino acid residue comprising an controduced and/or at least one removed amino acid residue comprising an control of the sold protein (IV) in at least one state). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least control of the surface, with the proviso that the comprising that the substitution is not fhr24sSer/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (C) gry202Ser/Ala/Thr/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr202Ser/Ala/Thr/His/Jys/Arg/Asn/Asp/Glu/Gly/Gln, (Z) a mucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (5) increasing (M2) the functional in vivo halfcress special conjugates, wariants for the treatment (and conjugates have an increased in conjugate and alpha-1 conformation of stroke, myocardial infarction such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased serum half-life, increased resistant to inhibitors, reduced conjugates have an increased in vivo half-life.

Conformation control of advantages over the currently available conformation languages over the currently available included in the conjugate offers a number of advantages over the currently available conformation duration between infections.
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                                                                                                                                                                                                                                                                                                   Matches 418;
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page; 92pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                         Local
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121 APGYKLGDDLLQCHPAVKFPCGRPMKRMEKKRSHLKRDTEDQEDQVDPRLLDGKMTRRGD 180
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                                                                                                                                                                                                                           1 ANSFLEELRHSSLERBCIEBICOFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA 60
                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                   SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                 SICCGHGTCTDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                          ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                   Conservative
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99.8%;
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                                                                                                                                                                                                                                                                                                Score 2318; DB 5;
Pred. No. 7.5e-143;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                     Length 419;
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18-OCT-2000; 21-JUN-2001;

18-OCT-2000;

21-JUN-2001;

2001US-0300154P. 2001DK-0000970. 2000DK-00001560.

MAXYGEN APS.
MAXYGEN HOLDINGS LTD.

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

WPI; 2002-489875/52.

Andersen KV,

Pedersen

H,

Freskgaard PO;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravacular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Protein C zymogen protein mutant M338A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU99096 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sepsis; septic shock; embolism; pulmonary embolism; burn;
bone marrow transplantation; major surgery; trauma; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                 WO200232461-A2
                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                          15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPWVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYHSSREKEAKRNRTFVLNF1K1PVVPHNECSEVMSNMSSENMLCAGTLGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                  158.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                                                                                                                                                                                                                                                    /label= Light_chain
156. .157
                                                                                                                                                                                                                                                                                                          /note= "Wild-type Met substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                           /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                    _abel= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                  .169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hurn; pregnancy; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
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Example 5; Page; 92pp; English

CC comprising (V) or (VI), (S) increasing (VZ) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The CC compugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and C diagnosis/prevention) of stroke, myocardial infarction, after venous CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 cc increased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreases, reduced immunogenicity and/or increased bloavailability. CC The conjugates protein, and fewer side effects. Moreover, a cc defining while maintaining the antiinflammatory activity of APC products, including longer duration between injections. Or administration of less protein, and fewer side effects. Moreover, a cc protein C vertein C conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is conjugate to the invention. Note: The present sequence is not conjugate has an extended plasma life. The gene for protein a zymogen containt of the invention of the sequence is not conjugate. attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (5) increasing (VX); the functional in vivo half-The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid residue comprising an introduced and/or at least one removed amino acid sequence which differs to a comprising an introduced and/or at least one removed amino acid sequence which differs to a comprising an amino acid sequence which differs to a parent protein C polypeptide (III) in at least one introduced amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising and acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which differs to a comprising an amino acid sequence which are comprising an amino acid sequence which are comprising an amino acid sequence which are comprising an am attached to

Sequence 419 AA; Local Similarity 99.7**%**; 99.8**%**; Score 2318; DB 5; Pred. No. 7.5e-143; DB 5; Length 419;

Matches 418;

Conservative

0;

Mismatches

Indels

0

Gaps

8 뮹 Q 61 1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 ب SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

61

SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120

SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI

240

Ş 뮹 R 밁 5 밁

181

GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP

S 뫄 8 밁

> AAU99032 standard; protein; 419 AA. AAU99032; 23-AUG-2002 (first entry)

Human Protein C zymogen protein mutant S250N/S252T

serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; prepancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; both transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein. Human; Protein C; N-glycosylation; APC; activated protein C; zymogen

Synthetic Homo sapiens.

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XX AAU99032
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O Misc-difference Misc-difference Protein Peptide Peptide Protein WO200232461-A2 252 250 158. /note= "Wild-type Ser substituted by Thr" /label= /label= Light\_chain Location/Qualifiers 'label= Heavy\_chain note= "wild-type Ser substituted by Asn" label= Activation\_peptide e1= Lys\_Arg\_dipeptide .419 . 169

15-OCT-2001; 2001WO-DK000679

18-OCT-2000; 2000DK-00001560. 18-OCT-2000; 2000US-0242268P. 21-JUN-2001; 2001DK-00000970. 21-JUN-2001; 2001US-0300154P.

(MAXY-) (MAXY-) MAXYGEN APS MAXYGEN HOLDINGS LTD

Andersen KV, Pedersen AH, Freskgaard PO;

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English

The invention relates to a conjugate (I) comprising at least one non-cc polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs CC from that of a parent protein C polypeptide (III) in at least one cc introduced and/or at least one removed amino acid residue comprising an CC extachment group for the non-polypeptide group (e.g. an N-glycosylation CC extachment group for the non-polypeptide group (e.g. an N-glycosylation CC extractivation in a position (P) where (P) is an amino acid with at least CC substitution in a position (P) where (P) is an amino acid with at least CC extractivation is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Gln/Cly/Cln, CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Gly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Gln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Cln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Tys/Arg/Asn/Asp/Cln/Cly/Cln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/CC Tyr3

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RBSULT 33
AAR1397
ID AAR13
XX AAR13
XC AAR13
XC DT 25-MA
DT 01-NC
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DE Human
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as ANU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, prespancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 419 AA;
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life or the serum half-life of a parent protein C polypeptide. The
conjugates, variants and protein C proteins are useful as medicaments,
and in the manufacture of medicaments for the treatment (and
                            HPC; thrombin; mutant
                                                                               Human protein C zymogen Q329
                                                                                                                                  25-MAR-2003
01-NOV-1991
                                                                                                                                                                                                                  AAR13997;
                                                                                                                                                                                                                                                                  AAR13997 standard; protein; 461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYHSSREKEAKRNRTFVLNPIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                (revised)
(first entry)
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99.5%;
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Pred. No. 7.5e-143;
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                                                                                                                                                                                                                                Matches 418;
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Best Local Similarity
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21-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 higher amidolytic and anticoagulant activity when activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-254443/35
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                                                                                                                                                                                                                                                                                          Sequence 461 AA;
181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCWDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                        103 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
                                                                            121
                                                                                                                                                                  43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                                                                                                           61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                         1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                       APGYKLGDDLLQCHPAVKEPCGREWKRMEKKRSHLKEDTEDQEDQVDPRLIDGKMTRRGD 180
                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDFRLIDGKMTRRGD
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90US-00628063.
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/label= AP
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/note= "light chain"
198. .199
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/note= "signal peptide and propeptide"
43. .197
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/note= "activated heavy chain"
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/note= "heavy chain"
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                                                                                                                                                                                                                                               Score 2318; DB 2;
Pred. No. 8.2e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein C zymogen Q097
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01-NOV-1991
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The zymogen forms of HPC represented in AAR13582, AAR13584, AAR13585 and AAR13597 have altered glycosylation patterns due to site-directed changes in the native HPC gene encoding the amino acid sequence. When activated, they have higher amidolytic and anticoagulant activity than the native
                                                                                                                                                                                                       23-FEB-1990;
21-DEC-1990;
                                                                                                                                                                                                                                            22-FEB-1991;
                                                              Claim 3; Page 28; 47pp; English.
                                                                                     Recombinant mutants of human protein c - with altered glycosylation for higher amidolytic and anticoagulant activity when activated.
                                                                                                                             WPI; 1991-254443/35.
                                                                                                                                                     Gerlitz BE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                     Grinnell BW;
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90US-00628063
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                                                                                                                                                                                                                                                                                                                                                                                 /label= HC
/note= "heavy chain"
200. .211
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "removed to form 200. .461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= pre-pro
/note= "signal peptide and propeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= LC
                                                                                                                                                                                                                                                                                                                                                         'note= "activation peptide'
                                                                                                                                                                                                                                                                                                                                label= AHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 461 AA;
                                                                                                                                                                      Key
Peptide
                                                                                                                                                                                                                                                                                   25-MAR-2003
01-NOV-1991
                                                                                                                                                                                                                                                                                                                           AAR13585;
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                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGYKIGDDLIQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLQCSLDNGGCTHYCLEEVGWRRCSC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SICCGHCTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEV//SNMVSENMLCAGIIGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                                                                                                                                                                                                                                                                                                                                                                                                              GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVEVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCNDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWTHGHIRDKEAPQKSWAP 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                           /label= HC
/note= "heavy
                                                                                                                                             /note= "signal peptide
                                                                                                                                                                                   Location/Qualifiers
                      /label=
                                                                                 /note=
                                                                                                                        /label= LC
                                                                                                         'note= "light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.7%;
99.8%;
                                                                                                                                .197
                                                                                               .199
                                  .211
                                                                     .461
         "activation peptide"
                                                                                   "removed to form 2-chain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 8.2e-143;
0; Mismatches 1;
                                              chain'
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RESULT 36
AAR13584
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The zymogen forms of HPC represented in AAR13582, AAR13584, AAR13585 and AAR13997 have altered glycosylation patterns due to site-directed changes in the native HPC gene encoding the amino acid sequence. When activated, they have higher amidolytic and anticoagulant activity than the native form and opt. increased affinity for thrombin. E. coli K12 AG1[pLPC-Q313 (NRRL B-18610) was obtained contg. the gene coding for the Aan-355-Gln mutation. pLPC-Q313 was recovered to transform 293 cells which were cultured to produce the zymogen mutant. The mutant had an amidolytic activity of 52 units/mg and anticoagulant activity of 627 units/mg compared to 35 units/mg and 325 units/mg respectively for wild-type activated HPC. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant mutants of human protein C - with altered glycosylation higher amidolytic and anticoagulant activity when activated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-254443/35
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21-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIL ) LILLY & CO ELI.
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                                                                                                 361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                    APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                                                                                                                                                        APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                     SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                   GYHSSREKEAKRORTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 402
                                                                                                                                                                     GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                   GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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90US-00628063.
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/label= AHC
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Pred. No. 8.2e-143;
0; Mismatches 1;
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43

1 ANSPLEELRHSSLEKECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

Matches Query Match Best Local S

418;

Conservative

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Score 2318; DB 2; Pred. No. 8.2e-143; 0; Mismatches 1;

Length 461; Indels

0;

Gaps

Similarity

99.7%;

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25-MAR-2003
01-NOV-1991
                     AARI3997 have altered glycosylation patterns due to site-directed changes in the native HPC gene encoding the amino acid sequence. When activated, they have higher amidolytic and anticoagulant activity than the native form and opt. incresased affinity for thrombin. E. coli Kl2 AGI/pLPC-Q248 (NRRL B-1869) was obtained contg. the gene coding for the Asn-248-Gln mutation. pLPC-Q248 was recovered to transform 293 cells which were cultured to produce the zymogen mutant. The mutant had an amidolytic activity of 63 units/mg and anticoagulant activity of 669 units/mg and compared to 35 units/mg and 325 units/mg respectively for wild-type activated HPC. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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21-DEC-1990;
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                                                                                                                                                                                                                                                                   Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                         22-FEB-1991;
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Sequence 461 AA;
                                                                                                                                      The zymogen forms of HPC represented in AAR13582, AAR13584, AAR13585 and AAR13997 have altered glycosylation patterns due to site-directed chance.
                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                            (ELIL ) LILLY & CO ELI.
                                                                                                                                                                           5; Page 28; 47pp; English.
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90US-00628063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200. .211
/label= AP
/note= "activation peptide"
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/note= "signal
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "activated heavy chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= LC
'note= "light chain"
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ARESULT 37
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24-SEP-1993
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                                                         18-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                         91US-00793989
                                                                                              92WO-US010242
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                                                                                                                                                                                                                                                                                                                                                                                             /note=
266. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
158. .1
                                                                                                                                                                                                                /note= "pref. PC polypeptide; claim 2, page 136"
390. .404
/note= "exosite 1; claim 1, page 136"
                                                                                                                                                                                                                                                                                                                 with fragment 266-287" 311. .331
                                                                                                                                                                                                                                                                                                                                                      /note= "claim 5, page 137
reacts with PC; fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "protein C activation"
170. .419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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.169
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                                                                                                                                                                                                                                                                            . 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "protein C light chain"
                                                                                                                                                                                                                                                                                            "exosite 2"
                                                                                                                                                                                                                                                                                                                                                                                                                "protein C heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC polypeptide; claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                      , page 137 describes an antibody that fragments 311-325 and 142-155 but not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            page
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microM. NB: Sequences corresp. to SBQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SBQUENCE LISTING. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 124-126; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-182244/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffin JH, Mesters RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                             181
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361
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                        GGPMVASFHGTWFLVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNWVSENMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                                                                   SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                         APGYKIGDDILLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                     SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA 60
                                                                                                                                      KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                KEVFVHPNYSKSTTDNDIALLHLAQPATISQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                    GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMGKKRSHLKRDTEDQEDQVDPRL1DGKMTRRGD
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2317; DB 2;
Pred. No. 8.7e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                       sepsis; septic shock; embolism; pulmonary embolism; burn; bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-l antitrypsin;
                                                                                                                                                                                           Human Protein C zymogen protein mutant H303N
                                                                                                                                                                                                                                                                                           AAU99047 standard; protein; 419
                                            Homo sapiens.
                                                                                                                                                                                                                             23-AUG-2002
                                                                                                                                                                                                                            (first entry)
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Key

Location/Qualifiers

mutant; mutein. pregnancy; coagulant;

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cc attachment group for the non-polypeptide group (e.g. an N-glycosylation co site). Also included are (1) a variant (IV) of [II] comprising a substitution in a position (P) where (P) is an amino acid with at least cc substitution in a position (P) where (P) is an amino acid with at least cc substitution in a position (P) where (P) is an amino acid with at least cc substitution is not Thr245Ser/Ala/His/Lyg/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (W); (4) a host cell (VII) (C) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cc life or the serum half-life of a parent protein C polypeptide. The cc onjugates, variants and protein C proteins are useful as medicaments, conjugates, variants and protein C proteins are useful as medicaments, cc adiagnosis/prevention) of stroke, myocardial infarction, after venous ct thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow creations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                        transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pedersen AH, Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Heavy_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           el= Lys_Arg_dipeptide
_419
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APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Mote: The greent sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9

15-OCT-2001; 2001WO-DK000679.

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RESULT 39
AAU99069
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                                                                                                                                                                                                                                                                                                                                  Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU99069 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protein C zymogen protein mutant V334N
                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGYKLGDDLLQCHPAVKFPCGRPWKRMBKKRSHLKRDTBDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYHSSREKEAKRURTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APGYKLGDDLLQCHPÄVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                      /note= "Wild-type Val substituted by Asn"
                                                                                                                                                                   /label=
                                                                                                                                                                                              /label=
                                                                                                                                                                                                                             /label=
                                                                                                                                     'label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.7%;
99.8%;
                                                                                                                                                   e1= Heavy_chain
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                                                                                                                                                                                              Lys_Arg_dipeptide
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    Mismatches

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Pred. No. 8.7e-143;
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CC Short its side group exposed to the surface, with the proviso that the CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding CC comparising (V) or (VI); (5) increasing (V2) the functional in vivo half-cc conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic cc shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult created serum half-life, increased in vivo half-life, increased intravascular to vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced CC renal clearance, reduced immunogenicity and/or increased bioavailability. CR products, including longer duration between injections, cadministration of less protein, and fewer side effects. Moreover, a conjugated enteries of conjugate and the infalmation activity is beneficial to reduce the risk of clastical notices. Constituted and conjugates are the smuch be expecially important when
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Best Local Similarity
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18-OCT-2000;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-489875/52.
                                                                                                                                                                                                                                                                                                                                                                                                                          located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
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                                                                                                                                                                                                                                                                                                                                                                                                                  protein C sequence appearing as AAU99002 and the information
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MAXYGEN HOLDINGS LTD.
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                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
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; 2001DK-0000970.
; 2001US-0300154P.
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Pred. No. 8.7e-143;
0; Mismatches 1;
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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18-OCT-2000; 2000US-0242268E.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154E.
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                                                WPI; 2002-489875/52
                                                                                                            (MAXY-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPWQVVILLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                             MAXYGEN APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                    /label= Activation_peptide
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

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Claim 9; Page; 92pp; English
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The invention relates to a conjugate (I) comprising at least one non-cc polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to cap protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one cintroduced and/or at least one removed amino acid sequence which differs c attachment group for the non-polypeptide group (e.g. an N-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising an substitution in a position (P) where (P) is an amino acid with at least CC substitution is not Thr24Ser/Ala/His/Hys/Arg/Asn/Asp/Glu/Gly/Gln, (CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or ph316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Ph316Ser/Ala/Thr/CC (TV); (3) an expression vector (VI) comprising (V) a host cell (VII) CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments for the treatment (and confidence of medicaments). CC diagnosis/prevention) of stroke, myocardial infartation, after venous cd diagnosis/prevention) of stroke, myocardial infartation (DIC), sepsis, septic cd thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic cd stock, emboli e.g. pulmonary emboli, transplantation such as bone marrow cd transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 cd antitrypsin. The conjugates have an increased in vivo half-life, increased in vivo half-life, renal clearance, reduced immunogenicity and/or increased bloavailability. The products, including longer duration between injections, cadministration of less protein, and fewer side effects. Moreover, a creduced anticoagulant activity is beneficial to reduce the risk of pleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is conjugate as a extended plasma life. The gene for protein C is shown in the specification but was created by the indexer using the conjugate as an annearing as an animanol and the indexer using the conjugate as an animal care and the indexer is not constant of the invention but was created by the indexer is not laim 4 constants in camerance ampearing as an animal and the information in claim 4 protein C sequence appearing as AAU99002 and the information in claim 9 419 AA;

Query Match Best Local Matches Local Similarity 417; Conservative 99.7%; 2; Score 2317; DB 5; Pred. No. 8.7e-143; Mismatches 0 Length 419; Indels 0; Gaps

δ Ś В Ş 밁 8 밁 멂 Ş Ś 361 301 241 181 181 121 121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180 61 61  $\vdash$  $\vdash$ SLCCGHGTCIDGIGS FSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA ANGFLEELRHSSLERBCIBEICDFEBAKEIFQNVDDTLAFWSKHVDGDQCLVLPLBHPCA SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI GYHSGREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS GYHSSREKEAKHNRTFVLNFIKIPVVPHNECSEVMSNMVSENNLCAGILGDRQDACEGDS 360 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD KEVFVHPNYSKNTSDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300 DSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240 240 120 60 60

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361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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AAU99075 standard; protein; AAU99075; Human Protein C zymogen protein mutant M338N 23-AUG-2002 (first entry) 419 ΑÃ

Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; bulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein. Homo sapiens

RESULT 41
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XX Augus Peptide Misc-difference Peptide Protein Synthetic Protein √1020023**2461-**A2 /note= "wild-type Met substituted by Asn" /label= Lys\_Arg\_dipeptide Location/Qualifiers /label= Light\_chain 'label= Activation\_peptide 'label= Heavy\_chain .419 .157 . 169

18-OCT-2000; 15-OCT-2001; 2001WO-DK000679 2000DK-00001560

18-OCT-2000; 21-JUN-2001; 21-JUN-2001; ; 2000US-0242268P. ; 2001DK-00000970. ; 2001US-0300154P.

(MAXY-) (-YXAM) MAXYGEN APS.
MAXYGEN HOLDINGS LTD

Andersen KV, Pedersen AH, Freskgaard PO;

WPI; 2002-489875/52

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English

polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an CC attachment group for the non-polypeptide group (e.g. an N-glycosylation substitution in a position (P) where (P) is an amino acid with at least CC site). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC state of the group exposed to the surface, with the provise that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/TC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) The invention relates to a conjugate (I) comprising at least one non-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2913-914. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
                                                                                                                                                                                                                                                                                                                                     23-AUG-2002
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein
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18-OCT-2000; 2000US-024226BP.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                      (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LID
                                                                                                                                                                                                                                                         Pedersen AH, Freskgaard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                               label= Light_chain
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                                                                                                                                                                                                                                                                                                                                                                                      Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                  Lys_Arg_dipeptide
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cc comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cc comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cc conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and cand in the manufacture of medicaments for the treatment (and chargosis/prevention) of stroke, myocardial infarction, after venous (cc diagnosis/prevention) of stroke, myocardial infarction, after venous (cc thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow (cc transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an (cc increased resistance to activation by e.g. human plasma and alpha-1 (cc antitrypsin. The conjugates have an increased in vivo half-life, increased complete (and complete attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln.
Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or bhe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an The invention relates to a conjugate (I) comprising at least one nonattached to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW25086 standard;
                             (-LTAd)
                                                                                                          30-NOV-1995;
13-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                         Key
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    blood clotting; anticoagulant; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein C; transgenic animal; sheep; rabbit; cattle; goat; milk;
                                                                                                                                                                                            26-NOV-1996;
                                                                                                                                                                                                                                                    05-JUN-1997
                                                                                                                                                                                                                                                                                                             WO9720043-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                             ZYMOGENETICS INC. PPL THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGYKLGDDLLQCHPAVKPPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYHSSREKEAKRNRTPVLNPIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETNVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                          95US-00565074
96US-0019692P
                                                                                                                                                                                               96WO-US018866
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.7%;
                                                                                                                                                                                                                                                                                                                                                                  "two-chain cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o
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Pred. No. 8.7e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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protein C production with therapeutic
                                                                                                                  Production of protein C in transgenic animal - useful for high quantity
                                                                                                                               N-PSDB; AAT79723, AAT79724.
                                                                                                                                                  Prunkard DE;
                                                                                                                                                        Garner I,
                                                                                                                                      1997-310599/28
                                                                                                                                                        Cottingham I, Temperley SM,
                                                                                                              value.
                                                                                                                                                          Foster DC,
                                                                                                                                                          Sprecher
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gland of a host female animal; and (b) using the DNA construct to breed transgenic animal (esp. sheep, rabbit, cattle, goat) that produces protein C in its milk, at least 90% of the protein C being in the two-chain form. Modification of the protein C two-chain cleavage site (see AAW25085) improves the maturation of recombinant protein C from single producing recombinant human protein C in the milk of a transgenic animal involves: (a) providing a DNA construct comprising DNA encoding a secretion signal and a protein C propeptide, operably linked to DNA encoding two-chain cleavage site-modified protein C, the 2 DNA sequences being linked to elements required for protein C expression in a mammary Disclosure; Page 58-60; 99pp; English This polypeptide comprises human protein C. A claimed method for producing recombinant human protein C in the milk of a transgenic animal chain to two-chain ρι

Sequence 460 AA;

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                                                              103
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                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                               418;
403
                              361
                                                               343
                                                                                                                             283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWA 418
                                                                                                                                                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPÄVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                    SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                                             GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99., F1
100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2317; DB 2; 1
Pred. No. 9.5e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
        460
                                                                                                       360
                                                                                                                                      342
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AAU99013
ID AAU
RESULT 44
                                Human Protein C zymogen protein mutant K193N/A195S.
                                                                          AAU99013 standard; protein;
                                               23-AUG-2002
                                               (first entry)
                                                                            419
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;

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cc site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the cc substitution is not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (T) a not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (T) a nucleotide sequence (V) encoding (C (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C comprising (V) or (VI); (5) increasing (V) the functional in vivo half-CC (Ife or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and CC diagnosis/prevention) of stroke, myocardial infarction, after venous chook, emboli e.g. pulmonary emboli, transplantation such as bone marrow matter accordance and the marrow matter than the marrow and the marrow and the marrow matter than such as bone marrow contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200232461-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                       transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bovavilability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an oacid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               attached to protein C polypeptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-489875/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Lys_Arg_dipeptide
158. .419
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protein,
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    and fewer side effects. Moreover, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMBKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                           SICCGHGTCIDGIGSESCDCRSGWEGRECQREVSELNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                          SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                               GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                      KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVFICLFDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                       SPWQVVLLDSKKNLSCGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.7%;

    Mismatches

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Pred. No. 1
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RESULT 45
AAU99019
Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                            AAU99019 standard; protein; 419
       Peptide
                                                                                                                                                                         sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mu
                                                                                                                                                                                                                                                                           Human Protein C zymogen protein mutant S216N/K218S
                                                                                                                                                                                                                                                                                                                                  AAU99019;
                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                        23-AUG-2002
                                     Protein
                                                              Peptide
                                                                                                                                                  Homo sapiens
                                                                                          Protein
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                       Location/Qualifiers
/label= Activation_peptide
                       /label= Heavy_chain
                                              /label= Lys_Arg_dipeptide
                                                                           /label=_Light_chain
                                                                   . 157
             .169
                                                                                                                                                                                   mutant; mutein
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Misc-difference

216

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cc attachment group for the mon-polypoptide group (e.g. an N-glycosylation cc site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least cc substitution in a position to the surface, with the proviso that the constitution is not Phr245Ser/Ala/His/Nry/Ary/Arn/Asp/Glu/Gly/Gln, (2) a muclaotide sequence (V) encoding cc Tyr302Ser/Ala/Thr/His/Iys/Ary/Ash/Asp/Glu/Gly/Gln, (2) a muclaotide sequence (V) encoding cc (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) cc (C); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) cc (C); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) cc (C); (3) an expression vector (VI); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (5) increasing (M2) the functional in vivo half-cc (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II); (II)
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001; 2001WO-DK000679
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                                                                                                                       The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced remain clearance, reduced immunogenicity and/or increased bioavailability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide moiety (II) (e.g. an N-glycosyl group) covalently atta
a protein C polypeptide comprising an amino acid sequence which di
from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a conjugate (I) comprising at least one non-
Sequence 419 AA;
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MAXYGEN
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Best Local Similarity 99. Matches 417; Conservative

99.7%;

Score 2316; DB 5; Pred. No. 1e-142; 1; Mismatches 1;

Length 419; Indels

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Gaps

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                        serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
18-OCT-2000;
18-OCT-2000;
21-JUN-2001;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                              sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein C zymogen protein mutant K308N/A310S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU99057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99057 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2002 (first entry)
                                                                                                                                 WO200232461-A2
                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                        Misc-difference 308
                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                          Кeу
                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                       15-OCT-2001; 2001WO-DK000679.
                                                                                                    25-APR-2002
                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDENKSLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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 ; 2000DK-00001560.
; 2000US-0242268P.
; 2001DK-0000970.
; 2001US-0300154P.
                                                                                                                                                                              310
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                              /label= Light_chain
                                                                                                                                                             /note= "Wild-type Ala substituted by Ser'
                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                         note= "Wild-type Lys substituted by Asn"
                                                                                                                                                                                                                        'label= Activation_peptide
                                                                                                                                                                                                                                                     label=
                                                                                                                                                                                                                                                                el= Lys_Arg_dipeptide
_419
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CC diagnosis/prevention) of stroke, myocardial infarction, after venous continuous is prevention) of stroke, myocardial infarction, after venous composis, emboli e.g. pulmonary emboli, transplantation such as bone marrow contractory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced confidences of conjugates have an increased in vivo half-life. The conjugates have an increased in vivo half-life, confidence of advantages over the currently available apoptation including longer duration between highering available apoptation including longer duration between highering available confidence anticoagulant activity is beneficial to reduce the risk of the conjugate has an extended plasma life. The gene for protein C incated on chromosome 2q13-q14. The present sequence represents a zymogen considered containt of the invention. Note: The present sequence is not confident confidence appearing as AAUS9002 and the information in claim 9 tx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment group for the non-polypoptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of [III] comprising a substitution in a position (P) where (P) is an amino acid with at least 5% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAXY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a conjugate (I) comprising at least one non-
polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached t
a protein C polypeptide comprising an amino acid sequence which differs
from that of a parent protein C polypeptide (III) in at least one
introduced and/or at least one removed amino acid residue comprising an
introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-489875/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   el conjugate useful for treating or preventing septic shock, stroke myocardial infarction, comprises non-polypeptide group covalently
181
                                         181
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                                                                                                                                                                                                                                                                                                                                                                 417;
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MAXYGEN HOLDINGS LTD.
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                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                          ANSFLEELRHSSLERECTEETCDFEBAKETFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
SPWQVVLLDSXKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                APGYKLGDDILQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                       99.7%;
                                                                                                                                                                                                                                                                                                                                                                 Score 2316; DB 5;
Pred. No. 1e-142;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 419;
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RESULT 47
AAU99007
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                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Protein C zymogen protein mutant $190N/K192S
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                                                                                                                                                                                                                                                                                                                                             Misc-difference 192
                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo gapiens.
                                                                                                                                                                                      18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                           Andersen KV, Pedersen AH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYHSSRENESKRURTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPWVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                    MAXYGEN APS.
MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     l. .135
/label=_Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Lys substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                        /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                         'note= "Wild-type Ser substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                 'label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                     er= rys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                 .169
                                                                                                                            Freskgaard PO;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

WPI; 2002-489875/52.

The invention relates to a conjugate (I) comprising at least one non-

Claim 9; Page; 92pp; English.

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           located on Chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 417; Conserv
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361
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GGPMVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAF 419
                                GGPMVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                           GYHS SREKEAKRNRTFVLNFIKI PVV PHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                     SPWQVVLLDNKSKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA
                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2316; DB 5
Pred. No. 1e-142;
1; Mismatches
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AAU99016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99016 standard; protein; 419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protein C zymogen protein mutant D214N/S216T
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                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Asp substituted by Asn" 216
                                                                                                                                                                                                                                                                                                                                                                                                   158.
                                                                                                                                                                                                                                                                                                                                                                                                       /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Ser substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                           /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Light_chain
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15-OCT-2001; 2001WO-DK000679

18-OCT-2000; 2000DK-00001560. 18-OCT-2000; 2000US-0242268P. 21-JUN-2001; 2001DK-00000970. 21-JUN-2001; 2001US-0300154P.

(MAXY-) (-YXAM) MAXYGEN HOLDINGS LTD. MAXYGEN APS

Š Pedersen AH, Freskgaard PO;

WPI; 2002-489875/52.

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

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attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr24Sser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a mucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, polypeptide moiety (II) (e.g., an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an The invention relates to a conjugate (I) comprising at least one non-

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RESULT 49
AAU99051
ID AAU99
XX AAU99
XX AAU99
XX Z3-AU
DT 23-AU
XX
DE Human
XX Human
XX Human
KW serum
KW serum
KW sepsei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC [activated protein C] conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 419
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                    sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                       serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC
                                                                                                                                                                                                                          23-AUG-2002
                                                                                                                                                                                                                                                                                                                      AAU99051 standard; protein; 419 AA
     adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein
                                                                                                                   Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                      Human Protein C zymogen protein mutant S305N/E307S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-024226BP.
21-UUN-2001; 2001DK-00000970.
21-UUN-2001; 2001US-0300154P.
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.419
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OSS XX REFERENCE XX REFERENCE FOR XX REFERENCE FOR THE FERENCE AND A CONTROL OF THE FERENCE FOR THE FERENCE FO

attached to protein C polypeptide comprising

Claim 9; Page; 92pp; English.

cc 25% of its side group exposed to the surface, with the provise that the cc 25% of its side group exposed to the surface, with the provise that the cc substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CTyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C comprising (V) or (VI); (5) increasing (V2) the functional in vivo half-cc life or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and C and in the manufacture of medicaments for the treatment (and C diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coapulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an C increased resistance to activation by e.g. human plasma and alpha-1 CC antitrypsin. The conjugates have an increased in vivo half-life, continuate offere a number of advantance over the currently availability. The conjugates have an increased in vivo half-life, antitrypsin. The configuates have an increased in vivo half-life, antitrypsin. The configuates have an increased in vivo half-life, antitrypsin. The configuates have an increased in vivo half-life, antitrypsin. The configuates have an increased in vivo half-life. attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC The invention relates to a conjugate (I) comprising at least one nonintroduced and/or at least one removed amino acid residue comprising an

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ARESULT 50
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ID AAU99995
AC AAU99
AC AAU99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                  sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
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                                                                                                                                                                                                                                                                                                                                                                                    C; N-glycosylation; APC; activated protein C; zymogen;
e; chromosome 2q13-q14; stroke; myocardial infarction;
                                                                                                    158.
                                                                                                                                                                                                  Location/Qualifiers
/note= "Wild-type Asp substituted by Ala"
                                                                                                                                        /label= Light_chain
156. .157
                                      /label= Activation_peptide
                                                                            /label= Heavy_chain
                                                                                                                     label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.7%;
                                                                                                  .419
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                                                                                                                   Lys_Arg_dipeptide
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Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                          burn; pregnancy;
ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                  coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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당 성

Query Match

99.7%;

Score 2316; UB 5; ... Pred. No. 1e-142;

Length 419; Indels

0,:

Conservative

1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA

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The invention relates to a conjugate (I) comprising at least one nonce of a protein c polypeptide comprising an amino acid sequence which differs that of a parent protein c polypeptide (III) in at least one introduced and/or at least one removed amino acid sequence which differs c from that of a parent protein c polypeptide (III) in at least one attachment group for the non-polypeptide group (e.g. an N-dycosylation cost pits). Also included are (1) a variant (IV) of (III) comprising an amino acid with at least the cost of the sits of group exposed to the surface, with the proviso that the cubit of the sits of group exposed to the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the cubit of the surface, with the proviso that the conjugates for the treatment (and cubit of the surface) and the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture of medicaments for the treatment (and cubit of the manufacture). The variant protein cubit of the surface of the subject of the subject of the subject of the subject of the subject of the subject of the subject of the subject of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000; 2000US-0242268P
21-JUN-2001; 2001DK-00000970
21-JUN-2001; 2001US-0300154P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001WO-DK000679
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Sequence 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C derivative 5.
          hypercoagulable states such as sepsis, disseminated intravascular coagulation, purpura fulminans, major trauma, major surgery, burns, adult respiratory distress syndrome, transplantation, deep vein thrombosis, heparin-induced thrombocytopenia, sickle cell disease, thalassemia, viral hemorrhagic fever, thrombotic thrombocytopenic purpura, and hemolytic uremic syndrome, and also useful for treating thrombotic disorders and acute coronary syndromes such as myocardial infarction, unstable angina, and stroke. Protein C derivatives with amino acid substitutions result in increased resistance to inacrivation by corries when communications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic disorders;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states predisposing thrombosis, comprises specific amino acid substitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerlitz BE, Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSUB;
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                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 49-51; 57pp; English.
                                                                                                                                                                                                                                                                               The present invention relates to a human protein C derivative. The protein is useful for treating vascular occlusive disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIL )
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Best Local Similarity Matches 417; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 419 AA;
                                                                                                                                                                                                                                                                   Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutant;
                                                                                                                                                                                                                                                                                                                                                                                Human Protein C zymogen protein mutant S190N/K192T
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                                                         Misc-difference
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                                        /note= "Wild-type Ser substituted by
                                                                                                                      /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                /label= Light_chain
                                                                                                                                                                                             Location/Qualifiers
                                                                         'label= Activation_peptide
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Pred. No. 1.
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/note= "Wild-type Lys substituted by Thr"

WO200232461-A2

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CC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to golypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to Cf a parent protein C polypeptide (III) in at least one controlled an amino acid sequence which differs introduced and/or at least one removed amino acid sequence which differs cattachment group for the non-polypeptide (III) in at least one controlled are (1) a variant (IV) of (III) comprising an estatachment group for the non-polypeptide group e.g. an N-glycosylation (2) substitution in a position (P) where (P) is an amino acid with at least the substitution is not "hri-45er/hla/His/Lys/Arg/Asn/Asp(dl), (IV) of (III) comprising a (IV), (I) an expression vector (IV) an unclectide sequence (V) encoding (IV), (I) an expression vector (IV) comprising (V); (A) a host cell (IVI) (CC life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosts, disseminated intravascular coagulation (DIC), sepsis, septic respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced immunogenicity and/or increased bioavailability. CC remain clearance, reduced immunogenicity and/or increased bioavailability. CC administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintening the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein a zymogen cc shown in the specification but was created by the indexer using the protein C sequence appearing as ANU99002 and the information in claim 9
                                        В
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                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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18-OCT-2000; 2000US-0242268P-
21-JUN-2001; 2001DK-00000970.
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                                                                                                                                                                                                             Sequence 419 AA;
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                                                                                                                                                 Similarity
SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                   ANSFLEELRHSSLERECIEEICDFEEAXEIFONVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
                                     ANSFLEEDRHSSLERECIEETCDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                          1;
                                                                                                                          Score 2315; DB 5;
Pred. No. 1.2e-142;
1; Mismatches 1;
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Andersen KV,

Pedersen AH,

Freskgaard PO

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                                                                                                                                                                                                                                                                                                                                              Peptide
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18-OCT-2000;
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                                                                                21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTBDQEDQVDPRLIDGKMTRRGD
                           MAXYGEN APS.
MAXYGEN HOLDINGS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVFYHPNYSKSTTUNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLYTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                   ; 2000DK-00001560.
; 2000US-0242268P.
; 2001DK-00000970.
; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                      /note= "Wild-type Arg substituted by Ser'
                                                                                                                                                                                                                                                                                                                                                              /label= Light_chain
                                                                                                                                                                                                                                                  note= "Wild-type Ser substituted by Asn"
                                                                                                                                                                                                                                                                                                        'label= Heavy_chain
                                                                                                                                                                                                                                                                             label= Activation_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic the coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic the coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (DIC), sepsis, septic coagulation (D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a conjugate (I) comprising at least one non-
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCWDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                  SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                          SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERBLNQAGQETLVTGW
                                                         KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
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Pred. No. 1.2e-142;
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RESULT 54
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CCCCCCXXXPTPTXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein C zymogen protein mutant $336N/M338T
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                                                                                                                      Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                            18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-024226BP.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                               Claim 9; Page; 92pp; English
                                                                                                                                                                                                           Andersen KV,
                                                                                                                                                                                                                                      (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GYHSSREKEAKRURTFYLNFIKIPVVPHNECSEVWSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein C; N-glycosylation; APC; activated protein C; zymogen;
half-life; chromosome 2q13-q14; stroke; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                           Pedersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                    338
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Met substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Ser substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label=
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                                                                                                                                                                                                           AH, Freskgaard PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy_chain
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polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation).

The invention relates to a conjugate (I) comprising at least one non-

sequence which differs

Human, Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;

Human Protein C zymogen protein mutant S304N/R306T

23-AUG-2002 (first entry)

sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.

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Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding
(IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII)
comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
life or the serum half-life of a parent protein C polypeptide. The
conjugates, variants and protein C proteins are useful as medicaments,
and in the manufacture of medicaments for the treatment (and
diagnosis/prevention) of stroke, myocardial infarction, after venous
thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic
shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
transplantation, burns, pregnancy, major surgery/trauma or adult
respiratory distress syndrome (ARDS). The variant protein C has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 417; Conservative
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substitution in a position (P) where (P) is an amino acid with at least
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                             GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMNTVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                          GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS
                                                                                                                                                                                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDILQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                    KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQBTLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŚPWQVVLLDŚKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2315; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 419;
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18-OCT-2000; 2000DK-00001550.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                    Misc-difference 306
                                                                                                                                                                                                                                                                                                                  Misc-difference 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                      25-APR-2002
                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
Andersen KV, Pedersen AH,
                                                                                                                                                                    15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                     WO200232461-A2
                                 (MAXY-)
                                                 (MAXY-)
                                   MAXYGEN HOLDINGS LTD
                                                  MAXYGEN APS
                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                   /note= "Wild-type Arg substituted by Thr
                                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                     /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                    note= "Wild-type Ser substituted by Asn"
                                                                                                                                                                                                                                                                                                                                      'label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                   .419
                                                                                                                                                                                                                                                                                                                                                                                                                      .157
                                                                                                                                                                                                                                                                                                                                                     .169
                                                                                                                                                                                                                                                                                                                                                                     Heavy_chain
 Freskgaard
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

WPI; 2002-489875/52.

Claim 9; Page; 92pp; English.

The invention relates to a conjugate (I) comprising at least one nonpolypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
a protein C polypeptide comprising an amino acid sequence which differs
from that of a parent protein C polypeptide (III) in at least one
introduced and/or at least one removed amino acid residue comprising an
attachment group for the non-polypeptide group (e.g. an N-glycosylation
site). Also included are (1) a variant (IV) of (III) comprising an
substitution in a position (P) where (P) is an amino acid with at least
Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding
(IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII)
comprising (V) or (VI); (5) increasing (W2) the functional in vivo halflife or the serum half-life of a parent protein C polypeptide. The
conjugates, variants and protein C proteins are useful as medicaments,
thrombosis/prevention) of stroke, myocardial infarction, after venous
thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic
shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
transplantation, burns, pregnancy, major surgery/trauma or adult

XAX

AAU99050;

AAU99050 standard; protein; 419 AA

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8888888888888888888888888888
RESULT 56
AAU99020
ID AAU99
AC AAU99
AC AAU99
XX 23-AU
XX 23-AU
XX Human
XX Human
KW Serum
KW Serum
KW Serum
KW Sepsi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, reduced anticoagulant activity is beneficial to reduce the risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                                                                         Human Protein C zymogen protein mutant S216N/K218T
                                                                                                                                                                                                                                                                                                                                                                                        AAU99020 standard; protein; 419 AA
                                                                                                   after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                    23-AUG-2002
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                                                                                                                                                                                       Protein C; N-glycosylation; APC; activated protein C; zymogen; half-life; chromosome 2q13-q14; stroke; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLEETRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLERLRHSSLERECIERICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGYKLGDDLLQCHPAVKPPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHNSTEKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2315;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
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Synthetic

Location/Qualifiers

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555555555
cc site). Also included are (1) a variant (IV) of [11] comprising a substitution in a position (P) where (P) is an amino acid with at least C25 of its side group exposed to the surface, with the proviso that the C25 of its side group exposed to the surface, with the proviso that the C25 of its side group exposed to the surface, with the proviso that the C25 of its of its side group exposed to the surface, with the proviso that the C25 of its of its side group exposed to the surface, with the proviso that the C25 of its or its earn and its side group and colored to the sequence (V) encoding C2 (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C2 comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-C2 conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and C2 conjugates, variants and protein C proteins are useful as medicaments, comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-C2 cand in the manufacture of medicaments for the treatment (and C2 cand in the manufacture of medicaments for the treatment (and C3 shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow C3 shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow C4 transplantation, burns, pregnancy, major surgery/trauma or adult canceased resistance to activation by e.g. human plasma and alpha-1 canceased resistance to activation by e.g. human plasma and alpha-1 canceased serum half-life, increased resistant to inhibitors, reduced canceased immunogenicity and/or increased bioavailable canceased serum half-life, increased resistant to inhibitors, reduced canceased serum half-life, increased resistant to inhibitors, reduced canceased serum half-life, increased over the currently available canceased serum half-life, increased resistant to inhibitors, reduced canceased serum half-life, increased serum between injections, cand dispersion of the conjugate has an extended plasma life. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a site).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-489875/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MAXY-) MAXYGEN HOLDINGS LTD
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/label= Light_chain
156. .157
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/label= Heavy_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                            Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Protein C zymogen protein mutant K308N/A310T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99058 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                          sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                    WO200232461-A2
                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDENKTLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQXSWAP
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                                                                                                                                                           /label= Heavy_chain
                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                  /label= Light_chain
                                                    /note= "Wild-type Ala substituted by Thr"
                                                                                       note= "Wild-type Lys substituted by Asn"
                                                                                                                           label= Activation_peptide
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Pred. No. 1.2e-142;
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61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC Ś

1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA

Query Match Best Local Similarity Matches 417;

99.6%;

Score 2315; Db 5; Pred. No. 1.2e-142; Pred. No. 1.2e-142;

Length 419; Indels

0;

60 60

120

Conservative

Sequence 419 AA;

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csubstitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not 'fir245Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln, CC Tyr302Ser/Ala/Th/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln, CC Tyr302Ser/Ala/Th/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (V1) comprising (V); (4) a host cell (V1) comprising (V) or (V1); (5) increasing (M2) the functional in vivo half-CC compusates, variants and protein C protein are useful as medicaments, CC and in the manifacture of medicaments for the treatment (and C diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coagulation (D1C), sepsis, septic c shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC respiratory distress syndrome (ARDS). The variant protein C has an CC increased resistance to activation by e.g. human plasma and alpha-1 CC antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced CC renal clearance, reduced immunogenicity and/or increased bioavailability. C administration of less nyotein, and fewer side effects. Moreover, a administration of less nyotein, and fewer side effects. Moreover, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-024226BP.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                       administration of less protein, and fewer side effects. Moreover, a reduced anticoagniant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a conjugate (1) comprising at least one non-polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page; 92pp; English.
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                  Andersen KV, Pedersen AH,
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                                                                                                                             (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD
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156. .157
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158. .419
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                                                              Freskgaard PO;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

The invention relates to a conjugate (I) comprising at least one non-CC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to CC a protein C polypeptide comprising an amino acid sequence which differs CT from that of a parent protein C polypeptide (III) in at least one CC introduced and/or at least one removed amino acid residue comprising an CC attachment group for the non-polypeptide group (e.g. an N-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising an CC substitution in a position (P) where (P) is an amino acid with at least CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the surface, with the proviso that the CC systematical conformation of the sequence (V) encoding (CIV); (3) an expression vector (VI) comprising (V) (4) a host volument (CIV); (3) an expression vector (VI) comprising (VI) (4) a host cell (VII) (COMPRISING (VI)); (3) an expression vector (VI) comprising (VI) (4) a host volument (VII); (5) increasing (VI) the functional in vivo half-CC interesting (VI); (3) an expression vector (VI) comprising (VI) as host voluments, (CIV); (3) an expression vector (VI) comprising (VI); (4) a host voluments, (VII); (5) increasing (VII); (5) increa located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a administration of less protein, and fewer side effects Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant procein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bloavailability.

Sequence 419 AA;

Query Match Best Local

Similarity

99.6%;

Score 2315; DB 5; Pred. No. 1.2e-142;

Length 419;

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GYHSSREKEAKRNRTFVINFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRODACEGDS
                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                            Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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                                                                                                                                                  Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                  WPI; 2002-489875/52.
                                                                                                               The invention relates to a conjugate (I) comprising at least one non-
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RESULT 60 AAU99045

AAU99045 standard; protein; 419 AA

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                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                         KEVFVHPNYSKSTTDNDIALIHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                              GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                    GYHSSREKEAKRNRT FVLNF I KI PVVPHNECSEVMSNMVSENML CAGILGDRQDACEGDS
                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                        SPWQVVLLDSKKNLTCGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                   ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                         99.5%;
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                                                                                                                                                                                                                                                                                                                                           Score 2315;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                               Mismatches
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tches 2;
                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                     Length 419;
                                                                                                                                                                                                                                                                                                                                Indels
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                        sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Protein C zymogen protein mutant Y302N.
WO200232461-A2
                                                                                                                             Peptide
                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                   label= Heavy_chain
                                                                                                                                                                                                                                                      'label= Light_chain
                                           note= "Wild-type Tyr substituted by Asn"
                                                                                               label= Activation_peptide
                                                                                                                                .169
                                                                                                                                                                                 .419
                                                                                                                                                                                                                                   .157
                                                                                                                                                                                                       Lys_Arg_dipeptide
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18-OCT-2000; 2000DK-00001560. 18-OCT-2000; 2000US-0242268P. 21-JUN-2001; 2001DK-00000970. 21-JUN-2001; 2001US-0300154P. MAXYGEN MAXYGEN APS. HOLDINGS LTD

15-OCT-2001; 2001WO-DK000679

Pedersen AH, Freskgaard PO;

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English

CC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to Ca protein C polypeptide comprising an amino acid sequence which differs C from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an CC attachment group for the non-polypeptide group (e.g. an N-glycosylation CS site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC comprising (V) or (VI); (5) increasing (WI) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and contents). diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced The invention relates to a conjugate (I) comprising at least one non-

Key

Synthetic

Peptide Protein

/label= Lys\_Arg\_dipeptide /label= Light\_chain 156. .157 Location/Qualifiers

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Matches 418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagniant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 419 AA;
                                                                                                                                                                           sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                      Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                       Human Protein C zymogen protein mutant S305N/E307T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU99052 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2002
                                                                                                                                     iomo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 1.2e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 419;
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CC 25% of its side group exposed to the surface, with the provise that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (Y) encoding CC (IY); (3) an expression vector (VI) comprising (Y); (4) a host cell (VII) CC comprising (Y) or (VI); (5) increasing (M2) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and Cd diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic csnock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 conjugate strance to activation by e.g. human plasma and alpha-1 confused serum half-life, increased resistant to inhibitors, reduced confused serum half-life, increased resistant to inhibitors, reduced confused serum half-life, increased resistant to inhibitors, reduced confused serum half-life, increased resistant to inhibitors, reduced confused serum half-life, increased resistant to inhibitors, reduced confused on clearance, reduced immunogenicity and/or increased bioavailability. The conjugate protein, and fewer side effects. Noreover, a confused products, including longer duration between injections, administration of less protein, and fewer side effects. Noreover, a confused protein C sequence 2013-9014 the present sequence the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C onjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is noted to confuse the confuse of the present sequence is not shown 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page; 92pp; English
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21-JUN-2001; 2001DK-00000970
21-JUN-2001; 2001US-0300154P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a conjugate (I) comprising at least one non-
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(MAXY-) MAXYGEN HOLDINGS LTD.
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18-OCT-2000; 2000US-0242268P.
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307
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/label= Heavy_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Activation_peptide
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Sequence 419 AA

15-OCT-2001; 2001WO-DK000679

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                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Protein C zymogen protein mutant K251N/T253S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU99034 standard; protein;
                                               25-APR-2002
                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                            WO200232461-A2
                                                                                                                                                                                                                                                                                                                                                                                   ndult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYHSNRTKEAKRIRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
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                                                                                                                                                                                           158.
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                          /note= "Wild-type Thr substituted by Ser"
                                                                                                                                          note= "Wild-type Lys substituted by Asn"
                                                                                                                                                                          /label= Activation_peptide
                                                                                                                                                                                                          'label=
                                                                                                                                                                                                                                         'label=
                                                                                                                                                                                                                                                           /label= Light_chain
156. .157
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                                                                                                                                                                                                    Heavy_chain
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Pred. No. 1.2e-142;
1; Mismatches 1;
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CC polypeptide moiety (II) (e.g. ann A-glycosyl group) covalently attached to compusing an amino acid sequence which differs controduced and/or at least one removed amino acid sequence which differs controduced and/or at least one removed amino acid sequence which differs controduced and/or at least one removed amino acid residue comprising an extrachment group for the non-polypeptide group (e.g. an N-glycosylation consists). Also included are (1) a variant (IV) of (III) comprising an extrachment group for the non-polypeptide group (e.g. an N-glycosylation consists). Also included are (1) a variant (IV) of (III) comprising a consist that the substitution is not thr245ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, comprising (N) an expression vector (VI) an amino acid with at least consuprising (N) and protein (1) an expression vector (VI) comprising (N) and protein (N) encoding (IV); (3) an expression vector (VI) comprising (N); (4) a host cell (VII) comprising (N) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and diagnosis/prevention) of stroke, myocardial infarction, after venous thromosis, disseminated intravascular coagulation (DIC), sepsis, septic conjugates, prepinacy, major surgery/trauma and alpha-1 conjugates, prepinacy, major surgery/trauma and alpha-1 conjugates have an increased in vivo half-life, confugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, conjugates have half-life, more and the pres
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18-OCT-2000;
21-JUN-2001;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page; 92pp; English.
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(MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                          Sequence 419 AA;
121
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                                                                                                                                                                                                                                                                            Similarity
                                                                                                           SICCGHGTCIDGIGSFSCDCRSGWBGRFCQRBVSFINCSIDNGGCTHYCLBBVGWRRCSC 120
                        APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                           ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNCGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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2000US-0242268P.
2001DK-0000970.
2001US-0300154P.
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    Mismatches

                                                                                                                                                                                                                                                                            Score 2315;
Pred. No. 1
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1.2e-142;
                                                                                                                                                                                                                                                                                                Length 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU99066 standard; protein; 419 AA
                                                                                                                                       18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                             /note= "Wild-type Thr substituted by Asn" Misc-difference 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Protein C zymogen protein mutant T315N/V317T
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                                                                                                                                                                                                          15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                           Andersen KV,
                                                                                                                                                                                                                                    25-APR-2002.
                                                 WPI; 2002-489875/52.
                                                                                                     (MAXY-)
                                                                                                                  (MAXY-)
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                                                                                                   MAXYGEN HOLDINGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSBNMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWBKWELDLDI 240
                                                                                                                  MAXYGEN APS
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                                                                            Pedersen
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                                                                                                                                                                                                                                                                                     /note= "Wild-type Val substituted by Thr"
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                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                    label= Light_chain
                                                                                                                                                                                                                                                                                                                                          label= Activation_peptide
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                                                                            ΑH,
                                                                                                                                                                                                                                                                                                                                                                 Heavy_chain
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                                                                            Freskgaard
                                                                               PO;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of [III] comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Th:245Ser/Ala/His/His/Lys/Arg/Asn/Asp/Gly/Gln, Tyr302Ser/Ala/Th:His/Lys/Arg/Asn/Asp/Gly/Gln or Phe316Ser/Ala/Th:His/Lys/Arg/Asn/Asp/Gly/Gln or Phe316Ser/Ala/Th:His/Lys/Arg/Asn/Asp/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) and the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and the treatment (via the conjugates). The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2413-614. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an Sequence 419 AA;

Matches 417; Conservative Query Match Local Similarity 99.6%; 0 Score 2315; DB 5; Pred. No. 1.2e-142; Mismatches 2 Length 419; Indels 0 Gaps 0:

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                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                    SPWQVVILLDSKKKLACGAVLIHPSWVIJTAAHCMDESKKLIVRLGEYDIRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                  GYHSSREKEAKRNRNFTLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                      GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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300
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Дb 64 361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419

AAB36897; AAB36897 standard; protein; 419 Human protein C derivative 4. 26-FEB-2001 (first entry

myocardial infarction; angina; stroke. Protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic disorders;

13-APR-2000; 2000WO-US008722 Homo sapiens. 30-APR-1999; 09-NOV-2000. 99US-0131801P

DR Protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states predisposing thrombosis, comprises specific amino acid substitutions. N-PSDB; AAC83314. WPI; 2001-007227/01. Gerlitz BE, Jones BE; (ELIL ) LILLY & CO ELI.

Claim 5; Page 48-49; 57pp; English

CC The present invention relates to a human protein C derivative. The CC protein is useful for treating vascular occlusive disorders, CC hypercoagulable states such as sepsis, disseminated intravascular (CC coagulation, purpura fulminans, major trauma, major surgery, burns, adult CC respiratory distress syndrome, transplantation, deep vein thrombosis, CC heparin-induced thrombocytopenia, sickle cell disease, thalassemia, viral CC temperine, thrombotic thrombocytopenic purpura, and hemolytic CC uremic syndrome, and also useful for treating thrombotic disorders and CC acute coronary syndromes such as myocardial infarction, unstable angina, CC and stroke, protein C derivatives with amino acid substitutions result in CC increased resistance to inactivation by serpins when compared to wild-CC type activated human protein C. They also have longer half-lives in human CC blood and hence require either less frequent administration and/or smaller dosage than wild type human protein C for treating disorders

Sequence 419 AA;

Query Match Best Local :

Similarity

99.6%;

Score 2314; Pred. No. 1

.4e-142; DB 4;

Length 419;

밁 S 밁 Q 밁 8 Matches 121 APGYKLGDDLLQCHPAVKFPCGRPWKNMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180 417; 61 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 ANSFLEELRHSSLERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA Conservative 1; Mismatches Indels 0 180 120 60

Claim 9; Page; 92pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coaquilation; DIC; sepsis; septic shock; embolism; purlmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-l antitrypsin; mutant; mut
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
          Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                     18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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                                                                                                                              MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                 Pedersen
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                                                                                                                                                                                                                                                                                                                                                          note= "Wild-type Asp substituted by Asn"
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Query Match Best Local Similarity

99.6**%**; 99.5**%**;

Pred. No. 1.4e-142; Score 2314; DB 5;

Length 419;

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cc substitution in a position (F) where (F) is an amino acto with the group exposed to the surface, with the proviso that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (Tyr302Ser/Ala/Thr/CC (Tyr302Ser/Ala/Thr/Asp/Glu/Gly/Gln, (Z) a nucleotide sequence (V) encoding (TV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C) comprising (V); (4) a host cell (VII) (C) comprising (V); (4) a host cell (VII) (C) ife or the serum half-life of a parent protein C polypeptide. The CC injugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and dagnosis/prevention) of stroke, myocardial infarction, after venous (C shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow (C transplantation, burns, pregnancy, major surgery/trauma or adult (Transplantation) to such a such a such a conjugates have an increased in vivo half-life, conjugates have an increased in vivo half-life, cantitrypsin. The conjugates have an increased in vivo half-life, cantitry such as conjugates over the courrently available (C APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a ceduced anticoagniant activity is bepteficial to reduce the risk of the conjugate has an extended plasma life. The gene for protein C is a clusted on chromosome 2q13-q14. The present sequence a symogen (C c protein C variant of the invention. Note: The present sequence is not constant of the invention. Note: The present sequence is not constant of the conjugates and ANJ99002 and the information in claim 9 crotein C sequence appearing as ANJ99002 and the information in claim 9 crotein C sequence appearing as ANJ99002 and the information in claim 9 crotein C sequence appearing as ANJ99002 and the information in claim 9 crotein constant of the constant of the constant of the constant of the constant of the constant of the const
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide mojety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a conjugate (I) comprising at least one non-
Sequence 419 AA;
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Ś В Ş 밁 S Ş Ş 문 8 맑 밁 밁 Matches 181 181 121 121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 361 301 301 241 241 417; Conservative 61 61 1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA 60 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNGSLDNGGCTHYCLEEVGWRRCSC 120 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 APGYKLGDDLLQCHPAVKFPCGRPWKRMBKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 GGPMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419 KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW SPWQVVLLNSSKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWBLDLDI SPWQVVLLDSKKKLACGAVLTHPSWVLTAAHCMDESKKLLVRLGEVDLRRWEKWELDLDI GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419 GYHSSREKEAKRNRTFVLNFIKI ÞVVÞHNECSEVMSNMVSENMLCAGILGDRQDACEGDS GYHSSREKEAKRNRT FVLNF IKIP VVPHNECSEVMSNMVSENMLCAGII GDRQDACEGDS KEVEVHENYSKSTTDNDIALLHLAQEATLSQTIVEICLEDSGLAERELNQAGQETLVTGW 300 Mismatches Indels 0 360 300 240 180 180 240 0

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18-OCT-2000;
21-JUN-2001;
21-JUN-2001;
                         polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a subscitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the subscitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, a mucleotide sequence (V) encoding this/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a mucleotide sequence (V) encoding the provisor of the subscitution of the subscitution of the subscitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, a mucleotide sequence (V) encoding the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of the subscitution of t
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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           (3)
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rg/msm/msp/stu/sty/stn; (2) a nucleotide sequence (V) encoding an expression vector (VI) comprising (V); (4) a host cell (VII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2c13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
life or the serum half-life of a parent protein C polypeptide. The
conjugates, variants and protein C proteins are useful as medicaments,
and in the manufacture of medicaments for the treatment (and
diagnosis/prevention) of stroke, myocardial infarction, after venous
thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors reduced renal clearance, reduced immunogenicity and/or increased bioavailability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 419 AA;
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                                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEÅPQKSWAP
                                                                                                                                                                                                                       KEVFVHENYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                    APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA
  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                          GYHSSREKEAKRNRTFYLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                      SPWQVVILDSKNKTACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                         KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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Pred. No. 1.4e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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RESULT 67
AAU99039
ID AAU99
XX AAU99039 standard; protein; 419

23-AUG-2002 (first entry)

Human Protein C zymogen protein mutant T254N/N256S

3222B2B28 Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;

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CC 25% of its side group exposed to the surface, with the proviso that the convergence of its side group exposed to the surface, with the proviso that the CC substitution is not Mhr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) and the proviso that the CC Tyri02Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) C comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and CC diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic Shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased serum half-life, increased in vivo half-life, increased serum half-life, increased in vivo half-life.

CC renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available of the conjugate offers and protein of the currently available of the conjugate offers and the currently available of the conjugate offers and the currently available of the conjugate offers and the currently available of the conjugate offers and the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently available of the currently avai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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18-CCT-2000; 2000US-024226BP.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a conjugate (I) comprising at least one non-
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APC products, including longer duration between injections
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                                                                                                                                                                                                                                                                           Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                      sepsis; septic shock; embolism; pulmonary embolism; burn; bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-l antitrypsin;
                                                                                                                                                                                                                                                                                                                                                     Human Protein C zymogen protein mutant M338N/S340T
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Pept ide
                                                                      Peptide
                                                                                                                                                                   Synthetic.
                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPMVAS FEGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYHSSREKEAKRNRTEVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRTFYLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                    /label= Light_chain
156. .157
                                                                                                                               Location/Qualifiers
               label= Heavy_chain
                                                 /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%;
 .169
                                   .419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2314; DB 5;
Pred. No. 1.4e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                             pregnancy;
coagulant;
                                                                                                                                                                                                                            mutant;
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Controduced and/or at least one removed amino acid residue comprising an catachment group for the non-polypeptide group (e.g. an N-glycosylation (c) site). Also included are (1) a variant (IV) of (III) comprising an constitution in a position (P) where (P) is an amino acid with at least (25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) an incleotide sequence (V) encoding (C) [IV; (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a host cell (VII); (4) a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Movel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen KV, Pedersen AH, Freskgaard PO;
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18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-2001; 2001WO-DK000679.
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338
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Query Match
Best Local Similarity
Matches 417; Conserv

Conservative

99.6%;

Score 2314; DB 5; Length 419; Pred. No. 1.4e-142; 1; Mismatches 1; Indels

0; Gaps

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ID AAU
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                                                                                                                                                                                                                                                                                                                                                                                               after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; sepsis rtransplantation, major surgery; trauma; ARDS; coagulant; bone marcow transplantation, major surgery; trauma; ARDS; coagulant; mutant; mutein.
 21-JUN-2001;
               18-OCT-2000;
18-OCT-2000;
                                                                                                                                                              Misc-difference
                                                                                                                                                                                          Misc-difference 189
                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Protein C zymogen protein mutant D189N/K191N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU99097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99097 standard; protein; 419 AA
                                                          15-0CT-2001;
                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNNVTENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGYKLGDDLIQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
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; 2000DK-00001560.
; 2000US-0242268P.
; 2001DK-00000970.
                                                          2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                       158.
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                             /note= "Wild-type Lys substituted by Asn'
                                                                                                                                                                                                                                                   158. .419
                                                                                                                                                                                                                                                                                          /label= Light_chain
                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                           note= "Wild-type Asp substituted by Asn'
                                                                                                                                                                                                         label=
                                                                                                                                                                                                                                                                             . 157
                                                                                                                                                                                                      Activation_peptide
                                                                                                                                                                                                                                 Heavy_chain
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CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleocide sequence (V) encoding (CC (TV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (4) a host cell (VII) comprising (VI); (5) a host cell (VII) comprising (VI); (5) a host cell (VII) comprising (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5) a host cell (VII); (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide moiety (II) (e.g. ann Aglycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the rysoloser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding the first conversion of the proviso and the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding the first conversion of the proviso that the surface (V) a host feel (VI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-489875/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAXY-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                          181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                   1 ANSFLEELRHSSLERBCIEBICDFERAKBIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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MAXYGEN HOLDINGS LTD
                                                                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                SLCCGHOTCIDGIGSESCDCRSGWEGRECOREVSELNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVSELNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2314; DB 5;
Pred. No. 1.4e-142;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 419;
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                             Claim 9; Page; 92pp; English
                                                                                                                                                                                                   WPI; 2002-489875/52
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                                                                                                                                                                                                                                                           Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                (MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                           (MAXY-) MAXYGEN APS
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156. .157
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; dissemined intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mut-
Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                            Pedersen AH, Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Lys substituted by Ser"
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polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to a protein c polypeptide comprising an amino acid sequence which differs c from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation controduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation control of the surface, with the proviso that the substitution in a position (P) where (P) is an amino acid with at least control of the surface, with the proviso that the constitution is not flnr245Ser/Ala/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln, (2) an substitution is not flnr245Ser/Ala/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Iys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (CIV); (3) an expression vector (V) comprising (V); (4) a host cell (VII) comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-cc infe or the serum half-life of a parent protein c polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, cand in the manufacture of medicaments for the treatment (and diamosis/nrevention) of stroke, myocardial inferretion after vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis/prevention) of stroke, myocardial infarction, after venous
thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic
shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
transplantation, burns, pregnancy, major surgery/trauma or adult
respiratory distress syndrome (ARDS). The variant protein C has an
increased resistance to activation by e.g. human plasma and alpha-1
antitrypsin. The conjugates have an increased in vivo half-life,
increased serum half-life, increased in vivo half-life.
increased serum half-life, increased resistant to inhibitors, reduced
renal clearance, reduced immunogenicity and/or increased bioavailability.
The conjugate offers a number of advantages over the currently available
APC products, including longer duration between injections,
administration of less protein, and fewer side effects. Moreover, a
ceduced anticoagulant activity is beneficial to reduce the risk of
bleeding while maintaining the antiinflammatory activity of APC
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2g13-g14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                  GGPMVASEHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANS FLEELRHS SLERECTEET COFEEAKETF QNVDDTLAFWS KHVDGDQCLVLPLEHPCA
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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Pred. No. 1.4e-142;
0; Mismatches 2;
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cc polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to ca protein C polypeptide comprising an amino acid sequence which differs cc from that of a parent protein C polypeptide (III) in at least one cintroduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation cc site). Also included are (1) a variant (IV) of (III) comprising a cc substitution in a position (P) where (P) is an amino acid with at least cc substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, cc substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, cc substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, cc Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a mucleotide sequence (V) encoding cc His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a mucleotide sequence (V) encoding cc (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) cc comprising (V); (5) increasing (M2) the functional in vivo half-cc life or the serum half-life of a parent protein C polypeptide. The

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Claim

9; Page; 92pp; English.

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

The invention relates to a conjugate (I) comprising at least one non-

WPI; 2002-489875/52

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AAU99022
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                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein C zymogen protein mutant K217N/L219T
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2001DK-00000970
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156. .157
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RESULT 72
AAU99070
ID AU99
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AC AAU99
XC AAU99
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Human
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Human
KW Serum
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myccardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagniant activity is beneficial to reduce the risk of bleeding while maintaining the antihiflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors, reduced
                                                                                                                                              Human Protein C zymogen protein mutant V334N/S336T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
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                                                                                                                                                                                             (first entry)
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Pred. No. 1.4e-142;
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18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-UUN-2001; 2001DK-00000970.
21-UUN-2001; 2001US-0300154P.
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WPI; 2002-489875/52.
                                      Andersen KV,
                                                                                                                                                                                                                                 15-OCT-2001; 2001WO-DK000679
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                                                                             (MAXY-) MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                   note= "Wild-type Val substituted by Asn"
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

CC from that of a parent protein (2 no) gape and annual sequence which date of a parent protein (2 no) and sequence which date of a parent protein (2 no) in at least one canonic (2 attachment group for the non-polypeptide group (e.g. an N-glycosylation (2 site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least (2 25% of its side group exposed to the surface, with the proviso that the cubstitution is not Thr245ser/Ala/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln (IV) (2 Ty302ser/Ala/Thr/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (2 comprising (V)) or (VI); (5) increasing (N2) the functional in vivo half-conjugates, variants and protein C protein are useful as medicaments, (2 and in the manufacture of medicaments for the treatment (and conjugates, variants and protein C proteins are useful as medicaments, (2 and in the manufacture of medicaments for the treatment (and conjugates) prevention) of stroke, myocardial infarction, after venous (2 thrombosis, disseminated intravascular coagulation such as bone marrow (2 transplantation, burns, pregnancy, major surgery/trauma or adult (2 increased resistance to activation by e.g. human plasma and alpha-1 (2 cantitrypsin. The conjugates have an increased in vivo half-life, increased in vivo half-life, increased is number of advantages over the currently available (2 administration of less protein, and fewer side effects. Moreover, a deministration of less protein, and fewer side effects. Moreover, a The invention relates to a conjugate (1) comprising at least one non-polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached a protein C polypeptide comprising an amino acid sequence which differs reduced anticoagulant activity is beneficial to reduce the risk of ç

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                                                                Protein
                                                                                                                                                                                                                                   sepers; seperc snock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKYSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVEVHDNYSKSTTDNDIALLHLAQPATUSQTIVPICLFDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSENMTNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                           156. .157
/label= Lys_Arg_dipeptide
158. .419
----- hain
                             /label=
158. .16
                                                                                                          1. .155
/label=_Light_chain
                                                                                                                                                Location/Qualifiers
                           eı= Heavy_chain
.169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2314; DB 5;
Pred. No. 1.4e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Misc-difference

351

/label= Activation\_peptide

Ş

1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

Query Match Best Local

Local

Similarity

99.5%;

Score 2314; DB 5; Pred. No. 1.4e-142; 1; Mismatches 1;

Length 419; Indels

0

Gaps

0

Conservative

Sequence 419 AA;

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CC 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,

CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/

CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (v) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (comprising (V)); (5) increasing (V2) the functional in vivo half-

CC conjugates, variants and protein C proteins are useful as medicaments, conjugates, variants and protein C proteins are useful as medicaments, conjugates, emboli e.g. pulmonary emboli, transplantation such as bone marrow concreased resistance to activation by e.g. human plasma and alpha-1 cantitypsin. The conjugates have an increased in vivo half-life, increased resistance to activation by e.g. human plasma and alpha-1 caminated serum half-life, increased resistant to inhibitors, reduced conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced conjugates have an increased in vivo half-life, increased protein conjugates have an increased in vivo half-life, administration of less protein, and fewer side effects. Moreover, a cadministration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity important when the conjugate has an extended plasma life. The gene for protein C is chown in the specification but was created by the indexer using the conjugate appearing as ANU99002 and the information in claim 9 the protein C sequence appearing as ANU99002 and the information in claim 9 the protein C leamn in claim 9 the protein C sequence appearing as ANU99002 and the information in claim 9 to the protein C leamn claim 9 the protein C leamn claim 9 the protein C leamn claim 9 the protein C leamn claim 9 the protein C leamn claim 9 the protein C lea
                                           attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000; 2000US-0242268P
21-JUN-2001; 2001DK-00000970
21-JUN-2001; 2001US-0300154P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Asp substituted by Asn" Nisc-difference 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000; 2000DK-00001560
18-OCT-2000; 2000US-0242268P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200232461-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAXY-) MAXYGEN APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92pp; English.
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RESULT 74
AAU99057
ID AAU99
XX AAU99
XX 23-AU
DT 23-AU
XX Human
XX Human
XX Homo
XX Serum
KW Serum
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                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Glu substituted by Asn" Misc-difference 309
                      18-CCT-2000; 2000DK-00001560.

18-CCT-2000; 2000US-024226BP.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Protein C zymogen protein mutant E307N/E309S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU99055 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                             WO200232461-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thromosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2002
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                                                                                                                                                                             15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Glu substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=_Lys_Arg_dipeptide
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
        protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                  The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                            Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                   Andersen KV, Pedersen AH, Freskgaard PO
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(MAXY-) MAXYGEN HOLDINGS LTD.
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                       181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
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                                                                                                                                                                                61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                    APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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Query Match Best Local .

Similarity

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Score 2314; DB 5; Pred. No. 1.4e-142;

Length 419;

Sequence 419

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                                                                                                                             Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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18-OCT-2000; 2000US-0242268P.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation, DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                          WPI; 2002-489875/52.
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                                                                                                                                                                                                                                                                                                                                                                        MAXYGEN APS.
MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                              Pedersen AH, Freskgaard PO;
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/note= "Wild-type Lys substituted by Ser"
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The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to

RESULT 76 AAU99024

Claim 9; Page; 92pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC a protein C polypeptide comprising an amino acid sequence which differs C from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an cattachment group for the non-polypeptide group (e.g. an N-glycosylation C site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least C 25% of its side group exposed to the surface, with the provise that the c substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, C Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) c comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The C conjugates, variants and protein C proteins are useful as medicaments, C diagnosis/prevention) of stroke, myocardial infarction, after venous c thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary embol, transplantation such as bone marrow marrow marrow marrow and the marrow cannot be considered that a company considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered considered conside
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplantation, burns, pregnancy, major surgery/traums or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-l antitrypsin. The conjugates have an increased in vivo half-life, intrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                       241 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERBLNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                   241 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 APGYKLGDDLLQCHPAVKFPCGRPWKKMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                GYHSSREKEAKRURTFYLNFIKIPYVPHNECSEVMSNMYSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDNSSKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2314; DB 5;
Pred. No. 1.4e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 419;
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attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not fhr24Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln or Ph23Ger/Ala/Thr/Firs/Arg/Asm/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or the serum half-life of a parent protein c polypeptide. The conjugates, variants and protein c proteins are useful as medicaments, and in the manufacture of medicaments for the textent (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                  The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                  Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99024 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                  Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-489875/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersen KV,
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21-JUN-2001; 2001DK-00000970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000; 2000DK-00001560.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein C zymogen protein mutant K218N/L220T
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the manufacture of medicaments for the treatment (and
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                  GGPMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                          GYHSSREKEAKHNRTFVLNFIKIPVVPHNBCSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 1.4e-142;
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AAU99053

AAU99053 standard; protein; 419 AA

AAU99053;

23-AUG-2002 (first entry)

Human Protein C zymogen protein mutant R306N/K308S

Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.

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ctatachment group for the non-polypoptide group (e.g. an M-glycosylation coste). Also included are (1) a variant [IV] of [II] comprising a substitution in a position (P) where (P) is an amino acid with at least C2 5% of its side group exposed to the surface, with the provise that the C2 5% of its side group exposed to the surface, with the provise that the C2 5% of its side group exposed to the surface, with the provise that the C3 5% of its side group exposed to the surface, with the provise that the C2 5% of its side group exposed to the surface, with the provise that the C3 5% of its side group exposed to the surface, with the provise that the C4 5% of its side group exposed to the surface, with the provise that the C4 5% of its side group exposed to the surface, with the provise that the cC4 fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fill of the fil
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18-OCT-2000;
21-JUN-2001;
21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached
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(activated protein C) conjugates. This must be especially important when
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158. .419
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156. .157
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                                  Human Protein C zymogen protein mutant E309N/K311S.
                                                                          23-AUG-2002
                                                                                                                                                  AAU99059 standard; protein; 419 AA
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Protein C; N-glycosylation; APC; activated protein C; zymogen
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Pred. No. 1.
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Misc-difference
                                                                                                                                                                          sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mu
                                                                                                                                                                                                           serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coaquiation; DIC;
                     Misc-difference
                                                               Protein
                                                                                     Peptide
                                                                                                            Protein
                                                                                                                     Key
                                         Peptide
                                                                                                                                            Synthetic
                                                                                                                                                      Homo sapiens
311
                     309
                                                                 158.
                                           158.
                                                                          /label=
                                                                                   /label= Light_chain
156. .157
                                                                                                                   Location/Qualifiers
          note=
                               /label=
                                                    /label= Heavy_chain
                                                             sı= Lys_Arg_dipeptide
_419
         "Wild-type Glu substituted by Asn"
                             Activation_peptide
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                                                                                                                                                                                           diagnosis/prevention) of stroke, myocardial infarction, after venous chrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow cransplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 complete and the conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced crenal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available cadministration of less protein, and fewer side effects. Moreover, a composite activity is beneficial to reduce the risk of bleeding while maintaining the antifilammatory activity important when the conjugate has an extended plasma life. The gene for protein C is coaded on chromosome 2013-914. The present sequence represents a zymogen composition of the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 xxx
                                                                                               Matches
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         substitution in a position (P) where (P) is an amino acid with at least 52% of its side group exposed to the surface, with the proviso that the substitution is not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and
                                                                                                                                                                                      Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel conjugate useful for and myocardial infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page; 92pp; English.
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                                                                                               Local Similarity
es 417; Conser
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MAXYGEN HOLDINGS LTD
ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                         ANSFLEELRHSSLERECIBEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
                                                                                            Conservative
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                                                                                                                  99.5%;
                                                                                                                                          99.6%;
                                                                                            0;
                                                                                       Score 2314; DB 5;
Pred. No. 1.4e-142;
0; Mismatches 2;
                                                                                                                .4e-142;
                                                                                                                                      Length 419;
                                                                                            Indels
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                                                                                       Gaps
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RESULT 79
AAU99048
ID AAU99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                  Misc-difference 305
                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU99048 standard; protein; 419 AA
(MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                 15-OCT-2001; 2001WD-DK000679
                                                                                                                                                                   25-APR-2002
                                                                                                                                                                                                 WO200232461-A2
                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKBAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDXEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 APGYKLGDDILQCHPÄVKEPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVL IHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                 303
                                                                                                                                                                                                                                                                                                                                                  /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                               /note= "Wild-type Ser substituted by Thr"
                                                                                                                                                                                                                                                                                                                                /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                               /label=_Light_chain
                                                                                                                                                                                                                                                              note= "Wild-type His substituted by Asn"
                                                                                                                                                                                                                                                                                               /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                     .157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25% of its side group exposed to the surface, with the provise that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, C) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (COMPRISING (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagglation (DIC), sepsis, septic chock embol's or "milmonary embol's transfirm and the protein of the conjugates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide moiety (II) (e.g. an N-alument)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                  241
                                                                                    181
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                                                                                                                                                                                                                                                                                                                                       61
KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                         SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                             SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2314; DB 5;
Pred. No. 1.4e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 419;
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RESULT 80
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The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-l antitrypsin; mutant; mut
                                                                                                         Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                 18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                              Claim 9; Page; 92pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                         WPI; 2002-489875/52.
                                                                                                                                                                                                                                                                                                                                                             15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Protein C; N-glycosylation; APC; activated protein C; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2002
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                                                                                                                                                                                                                                       MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                     MAXYGEN APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYNSTREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHSSREKEAKRNRIFYLNFIKIPYVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C zymogen protein mutant D172N/K174S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Lys substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Light_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Wild-type Asp substituted by Asn"
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                                                                                                                                                                                                      Freskgaard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (VI); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (2) comprising (V) or (VII); (5) increasing (W2) the functional in vivo half-comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polymeptide. The conjugates have an increased in vivo half-life, increased resistance transplantation (DIC), sepsis, septic concepts of the conjugates have an increased in vivo half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           remal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     introduced and/or at least one removed amino acid residue comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                181
       361
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                                                                                                                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDFRLIDGKWTRRGD 180
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                      GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEVDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                          GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS
                                                                                                                                                                                          KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                        KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLINGSMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
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Pred. No. 1.4e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 419;
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18-OCT-2000; 2000DX-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DX-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-l antitrypsin; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Protein C; N-glycosylation; APC; activated protein C; zymo serum half-life; chromosome 2q13-q14; stroke; myocardial infarcti after venous thrombosis; disseminated intravascular coagulation;
  Andersen KV,
                                                                                                                                                                                                                                                                15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                         WO200232461-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                              (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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Pedersen AH,
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                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Lys substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Lys_Arg_dipeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Activation_peptide
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Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APC; activated protein C; zymogen;
L4; stroke; myocardial infarction;
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WPI; 2002-489875/52.

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

CC The invention relates to a conjugate (I) comprising at least one nonCC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
CC a protein C polypeptide comprising an amino acid sequence which differs
CC from that of a parent protein C polypeptide (III) in at least one
CC introduced and/or at least one removed amino acid residue comprising an
CC attachment group for the non-polypeptide group (e.g. an N-glycosylation
CC site). Also included are (1) a variant (IV) of (III) comprising a
CC substitution in a position (P) where (P) is an amino acid with at least
CC substitution is not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding
CC (IV); (3) an expression vector (VI) comprising (V); (4) a bost cell (VII)
CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo halfCC (Iife or the serum half-life of a parent protein C polypeptide. The
CC conjugates, variants and protein C proteins are useful as medicaments,
CC and in the manufacture of medicaments for the treatment (and
CC diagnosis/prevention) of stroke, myocardial infarction, after venous
CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic

AAU99006 ID AAU9 XX

AAU99006 standard; protein; 419 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
         361
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                                                                                                                      GYHSSREKEAKRNRTFYLNFIKIPYVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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                                                                                                                                                                                                                                                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                    GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                         KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                    KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                               SPWQVVLLNSTKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANSFLEELRHSSLERECIEEICDFBEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 1.6e-
1; Mismatches
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RESULT 8
AAU9901A
AAU901A
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AC AAU9
AC AAU9
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AC AAU9
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DT 23-J
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Humm
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Addul
                                                  sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                     serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                Human Protein C zymogen protein mutant E215N/K217T
                                                                                                                                                                                                                                                                   23-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                         AAU99018 standard; protein; 419 AA
                                                                                                                                                                   Protein C; N-glycosylation; APC; activated protein C; zymogen;
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Synthetic

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18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
WPI; 2002-489875/52.
                                                                                                                                                                                                                             15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                               Misc-difference 217
                                    Andersen KV, Pedersen AH, Freskgaard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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(MAXY-) MAXYGEN HOLDINGS LTD.
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                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Lys substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Glu substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                    label= Activation_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                            .169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lys_Arg_dipeptide
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 cincreased serum half-life, increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced crenal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available cadministration of less protein, and fewer side effects. Moreover, a cadministration of less protein, and fewer side effects Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antinflammatory activity of all conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogem introduced and/or at least one removed amino acid residue comprising an cattachment group for the non-polypeptide group (e.g. an N-glycosylation cattachment group for the non-polypeptide group (e.g. an N-glycosylation cattachment group for the non-polypeptide group (e.g. an N-glycosylation cattachment group for the non-polypeptide group (e.g. an N-glycosylation cattachment group are possible to the surface, with the provising a substitution in a position (P) where (P) is an amino acid with at least cat for the surface, with the proviso that the substitution is not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CTyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CTyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CTV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (V); the functional in vivo half-composition (VI); (5) increasing (V); the functional in vivo half-composition (VI); (S) increasing (VI); (A) an expression vector (VI); (B) increasing (VI); (A) an expression vector (VI); (B) increasing (VI); (B) increasing (VI); (A) an expression vector (VI); (B) increasing (VI); polypeptide moiety (II) (e.g. an N-glycosyl group) a protein C polypeptide comprising an amino acid s from that of a parent protein C polypeptide (III) in at least one The invention relates to a conjugate (I) comprising at least one nonsequence which differs covalently attached to

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RESULT 83
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Best Local
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                                                         Misc-difference 255
                                                                                                                   Misc-difference
                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; some marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Protein C zymogen protein mutant T253N/D255S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU99037 standard; protein; 419 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult respiratory distress syndrome; alpha-1 antitrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDNSKTLLVRLGEYDLRRWEKWBLDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWEKWBLDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                   253
                   /note= "Wild-type Asp substituted by Ser
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                            note= "Wild-type Thr substituted by Asn"
                                                                                                                                                                                                         'label= Heavy_chain
                                                                                                                                         label= Activation_peptide
                                                                                                                                                                                                                                                                         label=
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Pred. No. 1
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9 묽 Q

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SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120

ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA

69

Matches 417; Query Match

Conservative

0; Mismatches Score 2313; DB 5; Pred. No. 1.6e-142;

Local Similarity

99.5%; 99.5%;

Length 419; Indels

0; Gaps

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                          CC increased resistance to activation by e.g. human plasma and alpha-1 CC antitypsin. The conjugates have an increased in vivo half-life, increased in vivo half-life increased serum half-life, increased in resistant to inhibitors, reduced concerned the conjugate offers a number of advantages over the currently available conjugate offers a number of advantages over the currently available conformation of less protein, and fewer side effects Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of the conjugate has an extended plasma life. The gene for protein C is conjugate has an extended plasma life. The gene for protein C is coated on chromosome 2q13-q14. The present sequence represents a zymogen content C variant of the invention. Note: The present sequence is not shown in the specification but was created by the information in claim 9 correctin C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                  Sequence 419 AA;
                                                                                                                                                                                                                                                                                             shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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   Andersen KV,
                                                                    18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                         15-OCT-2001; 2001WO-DK000679.
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                           MAXYGEN HOLDINGS LTD.
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 Pedersen AH,
                                                                                                                                                                                                                                                                                                                                  /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                              note= "Wild-type Arg substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                          /label=_Light_chain
                                                                                                                                                                                                                                                        note= "Wild-type Arg substituted by Asn"
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Freskgaard PO;
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CC Hys102ser/Ala/Thr/His/Lys/Arg/Ash/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (CC His/Lys/Arg/Ash/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (C (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-C comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-C comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-C conjugates, variants and protein C protein C polypeptide. The conjugates, wariants and protein C protein are useful as medicaments, and increasing (M2) the functional in vivo half-C conjugates, pregnancy myocardial infarction, after venous conformation, burns, pregnancy, major surgery/trauma or adult transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced conjugate offers a number of advantages over the currently available. The products, including longer duration between injections, reduced immunogenicity and/or increased bloavailability. The products, including the antihifilammatory activity of APC products, including the antihifilammatory activity of APC captivated protein C onjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 to the protein C sequence appearing as AAU99002 and the information in claim 9 to the protein C sequence appearing as AAU99002 and the information in claim 9 to the protein C sequence appearing as AAU99002 and the information in claim 9 to the protein C sequence is protein C sequence is not protein C sequence is not protein C sequence is not protein C sequence is not protein C sequence is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245ser/Ala/His/Lys/Arg/Aan/Aap/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Gly/Glu/Glu/Glu/G
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Matches 417;
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Best Local Similarity
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KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW
                                                                         SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                            APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                         SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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Pred. No. 1.6e-142;
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8 Дb Ş 밁 Ş

Sequence 419 AA;

Length 419;

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           The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99083 standard; protein; 419 AA
                                                                                                       Claim 9; Page; 92pp; English
                                                                                                                                                    Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently
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18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mu
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                                                                                                                                    attached to protein C polypeptide comprising an attachment group
                                                                                                                                                                                                     WPI; 2002-489875/52
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and/or at least one removed amino acid residue comprising an group for the non-polypeptide group (e.g. an N-glycosylation
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                                                                                                                                                                                                                                  Pedersen AH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Wild-type Asp substituted by Ser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Wild-type Arg substituted by Asn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC substitution in a position (P) where (P) is an amino acid with at least C25% of its side group exposed to the surface, with the proviso that the csubstitution is not Thr245Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe315Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe315Ser/Ala/Thr/CC (P) and the sequence (V) encoding (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (Comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC (1ife or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous (CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow (CC trespiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plaema and alpha-1 (CC increased serum half-life, increased resistant to inhibitors, reduced crenal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available (CC APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a cadivated protein C onjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is cover the invention but was created by the indexer using the cc shown in the specification but was created by the indexer using the cc shown in the specification but was created by the indexer using the cc shown in the specification but was created by the infermation in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate place in the created by the infermation in claim 9 to the conjugate place in the conjugate p
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSIDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSIDNGGCTHYCLEEVGWRRCSC 120
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                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQXSWAP 419
                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANSFLEELRHSSLERECIEEI CDFEEAKEI FQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                    GYHSSREKEAKRURTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDNQSACEGDS
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                                                                                                                                                                                                        KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQXSWAP
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Pred. No. 1.6e-142;
0; Mismatches 2;
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RESULT 86
AAU99021
ID AAU99021 standard; protein; 419 AA
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AC AAU99021;
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23-AUG-2002

(first entry)

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attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) its an amino acid with at least 55% of its side group exposed to the surface, with the proviso that the substitution is not fhr245Ser/Ala/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and discovered the server of medicaments for the treatment (and discovered the server of medicaments for the treatment (and discovered the server of medicaments for the treatment (and discovered the server of medicaments for the treatment (and discovered the server of medicaments).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2g13-g14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation, DIC;
thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult
                                                                                                                                       diagnosis/prevention) of stroke, myocardial infarction, after venous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    el conjugate useful for treating or preventing septic shock, stroke myocardial infarction, comprises non-polypeptide group covalently ached to protein C polypeptide comprising an attachment group.
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; 2000US-0242268P.
; 2001DK-00000970.
; 2001US-0300154P.
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                                                            GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                              GYHSSREKEAKHNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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Pred. No. 1
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nes 2;
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Human Protein C zymogen protein mutant D172N/K174T.

23-AUG-2002

(first entry)

Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein. pregnancy; coagulant;

Homo sapiens

Synthetic

Location/Qualifiers

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The invention relates to a conjugate (I) comprising at least one non-
CC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
CA a protein C polypeptide comprising an amino acid sequence which differs
CC from that of a parent protein C polypeptide (III) in at least one
CC introduced and/or at least one removed amino acid residue comprising an
CC attachment group for the non-polypeptide (III) in at least one
CC slte). Also included are (I) a variant (IV) of (III) comprising an
CC slte). Also included are (I) a variant (IV) of (III) comprising
CC 25% of its side group exposed to the surface, with the proviso that the
CC substitution is not Mnz4SSer/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a mucleotide sequence (V) encoding
CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII)
CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
CC conjugates, variants and protein C proteins are useful as medicaments,
CC diagnosis/prevention) of stroke, myocardial infarction, after venous
CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic
CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
CC transplantation, burns, pregnancy, major surgery/trauma or adult
CC respiratory distress syndrome (ARDS). The variant protein C has an
CC antitrypsin. The conjugates have an increased in vivo half-life,
CC increased serum half-life, increased resistant to inhibitors, reduced
CC the conjugate offers a number of advantages over the currently available
CC ARC products, including longer duration between injections.
                                                                                               APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial reduce the risk of bleeding while maintaining the antinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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MAXYGEN HOLDINGS LTD.
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172
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                WO200232461-A2
                                                              Misc-difference
                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Protein C zymogen protein mutant D255N/D257S.
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                                                                                              Misc-difference
                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                     adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
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                                                                                                                                158.
                                                                                                                                                             /label= Lys_Arg_dipeptide
158. 419
                                                                                                                                                                                                                                               Location/Qualifiers
                                              /note=
                                                                            note= "Wild-type Asp substituted by Asn"
                                                                                                           /label= Activation_peptide
                                                                                                                                             /label= Heavy_chain
                                                                                                                                                                                                               /label=_Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.5%;
                                                                                                                                .169
                                              "Wild-type Asp substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2313; DB 5;
Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 cc antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced cc increased serum half-life, increased resistant to inhibitors, reduced cc remal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available capc products, including longer duration between injections, capc products, including longer duration between injections, capc reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc attachment group for the non-polypeptide group (e.g. an N-glycosylation cc site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least cc substitution in a position to the surface, with the proviso that the cubstitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (C His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (C (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) (C comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cc or the serum half-life of a parent protein ( polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, C and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous controls are capacitated and controls are capacitated.
                                                                                                                                                                               Matches 417;
                                                                                                                                                                                                       Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Movel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2002
                                                                                                                                                                                                                                                                         Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                 located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-489875/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAXY-) MAXYGEN APS
61
                                                                                                                                    MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                       Similarity
SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                               ANS FLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA
                                                                                      ANSFLEELRHSSLERECIEEI CDFEEAKEI FQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000DK-00001560.
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                                                                                                                                                                           1,
                                                                                                                                                                                                   Score 2313; DB 5;
Pred. No. 1.6e-142;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                        Length 419;
                                                                                                                                                                               Indels
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                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pumonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; bdult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Protein C zymogen protein mutant R312N/R314T.
                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                         Andersen KV, Pedersen AH,
                                                                                                              21-JUN-2001;
                                                                                                                          18-OCT-2000;
18-OCT-2000;
                                                                                                                                                                      15-OCT-2001; 2001WO-DK000679
                                                                     (MAXY-)
                                                      (-YXAM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                      MAXYGEN HOLDINGS LTD
                                                                    MAXYGEN APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRT FVLNF I KLIPVVPHNECSEVMSNMVSBNMLCAGI LGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYHSSREKEAKRNRTEVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEVFVHPNYSKSTTNNS IALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEVEVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                               ; 2000US-0242268P.
; 2001DK-00000970.
; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                         2000DK-00001560
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                          /note= "Wild-type Arg substituted by Thr'
                                                                                                                                                                                                                                                                                                                 /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                             /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                   'label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                    /label= Light_chain
                                                                                                                                                                                                                                                                                    note= "Wild-type Arg substituted by Asn"
                                                                                                                                                                                                                                                                                                                                 . 169
                                                                                                                                                                                                                                                                                                                                                             .419
                           Freskgaard PO;
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WPI; 2002-489875/52

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substitution in a position (P) where (P) is an amino acid with at least (C 25% of its side group exposed to the surface, with the proviso that the substitution is not fhr24SSer/Ala/His/Lys/Arg/Asn/Asp/Glu/GlyGlyGln, C Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe31Ser/Ala/Thr/C His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial intarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow cresplantatory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-lation comprised service in the protein conjugates have an increased in vivo half-life, increased servin half-life increased in vivo half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is considered on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as ANU99002 and the information in claim 9 or the conjugate appearing as ANU99002 and the information in claim 9 or the present sequence is not content to the conjugate appearing as ANU99002 and the information in claim 9 or the present sequence is not conjugate the protein C sequence appearing as ANU99002 and the information in claim 9 or the present sequence is not conjugate the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C sequence appearing as ANU99002 and the information in claim 9 or the protein C 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide molety (II)
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301 GYHSSREKEAKRURIFVLNEIKIPVPPHNECSEVMSUMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGR.PWKRMEKKRSHLKR.DTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                             KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTTVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2313; DB 5;
Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an N-glycosyl group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 90
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            The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC sepsis; septic shock; embolism; pulmonary embolism; burn; pregmancy; bone marrow transplantation; major surgery; trauma; ARDS: coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2002
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                                                                                                                                                                                          Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                 18-DCT-2000; 2000DK-00001560.
18-DCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-0000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Protein C zymogen protein mutant D351N/Q353T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU99082 standard; protein; 419
                                                                                                                                                      Claim 9; Page; 92pp; English
                                                                                                                                                                                        attached to protein C polypeptide comprising
                                                                                                                                                                                                                                                             WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DCT-2001; 2001WO-DK000679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WD200232461-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                               Andersen KV,
                                                                                                                                                                                                                                                                                                                                  (MAXY-) MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                MAXYGEN APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                              Pedersen AH, Freskgaard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Gln substituted by Thr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=_Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Wild-type Asp substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Activation_peptide
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Human Protein C zymogen protein mutant K191N/K193T

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RESULT 91
AAU99010
ID AAU99
XX
AC AAU99
XZ
DT 23-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available approximation of the conjugate offers a number of advantages over the currently available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Hys/Arg/Asn/Asp/Glu/Gly/Gln/Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe31Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, 2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 419 AA;
                                                                                                                       AAU99010 standard; protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDUTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                                                                                                                                                  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKBAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGNRTDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERBLNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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cell (VII)
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18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                     (MAXY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Protein C; N-glycosylation; APC; activated protein C; zymogen; half-life; chromosome 2q13-q14; stroke; myocardial infarction; venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                             MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                     MAXYGEN APS
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                                                                                                                                                                                                                                                                             Pedersen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Lys substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Lys substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abel= Heavy_chain
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                                                                                                                                                                                                                                                                             AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activation_peptide
                                                                                                                                                                                                                                                                            Freskgaard PO;
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WPI; 2002-489875/52.

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

cc attachment group for the non-polypeptide group (e.g. an N-glycosylation cc site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least cc substitution in a position to the surface, with the proviso that the cubstitution is not fhr24SSer/Ala/His/Iys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a molectide sequence (V) encoding crising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (3) an expression of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and conjugates, variants and protein conjugates) after venous changes of thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow and the conjugates of the conjugates of the conjugates of the conjugates of the conjugates of the conjugates of the conjugates of the conjugates of manufacture of medicaments for the treatment (and conjugates) conjugates of medicaments for the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of the treatment (and conjugates) conjugates of medicaments of medicaments of medicaments of medicaments of medicaments of medicaments of medicaments of medicaments of medicaments of polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an shock, emboli e.g. pulmonary emboli, transplantation such as bone m transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-l The invention relates to a conjugate (I) comprising at least one non-

23-AUG-2002 AAU99010;

(first entry)

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RESULT 92
AAU99040
ID AAU99040
XX AAU99
AC AAU99
XX Human
XX Human
XX Human
XX Human
XX Human
XX Human
XX Human
XX Human
XX Human
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XX Human
XX Human
XX Serum
XX Serum
XX Sepsi
XX Seynth
XX FH Key
FT Prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                         sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 419 AA;
                                  Protein
                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                     serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                              Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protein C zymogen protein mutant T254N/N256T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99040 standard; protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPWQVVLLDSNKTLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
/label= Light_chain
                                                        Location/Qualifiers
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Pred. No. 1.6e-142;
0; Mismatches 2;
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                                                                                                                                                                                                                mutant; mutein.
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18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-024226BP.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                              WPI; 2002-489875/52
                                                                                                                                                                                                                                       Andersen KV,
                                                                                                                                                                                                                                                 (MAXY-)
                                                                                                                                                                                                                                                                                                            W0200232461-A2
                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                        15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                 MAXYGEN APS.
MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                      MAXYGEN
                                                                                                                                                                                                                                       Pedersen AH,
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                                                                                                                                                                                                                                                                                                                                                            /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                          /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                   /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Asn substituted by Thr"
                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Thr substituted by Asn'
                                                                                                                                                                                                                                                                                                                                               .169
                                                                                                                                                                                                                                       Freskgaard PO;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow contraining the property of transplantation, burns, pregnancy, major surgery/transma or adult respiratory distress syndrome (ARDS). The variant protein C has an contrained and increased resistance to activation by e.g. human plasma and alphal cantitypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced crenal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available capproducts, including longer duration between injections, cadministration of less protein, and fewer side effects. Noreover, a reduced anticoagallant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The greener for protein C is considered on chromosome 2q11-q14. The present sequence is not content of the invention but was created by the indexer using the more of the configuration but was created by the indexer using the content of the configuration but was created by the indexer using the cc introduced and/or at least one removed amino acid residue comprissing an CC attachment group for the non-polypeptide group (e.g. an N-glycosylation CC sibstitution in a position (i) a variant (IV) of (III) comprising a cubstitution in a position (p) where (p) is an amino acid with at least CC substitution in a position (p) where (p) is an amino acid with at least CC substitution is not Thr24Ser/Ala/His/Mrg/Asn/Asp/Glu/Gly/Gln, (r) a positivation of the surface, with the proviso that the CC substitution is not Thr24Ser/Ala/His/Mrg/Asn/Asp/Glu/Gly/Gln or Phe31Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe31Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic cohock smboli or villonnavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic cohock smboli or milmonavy macholi transplantation choice septic chock smboli or milmonavy macholi transplantation choice septic chock smboli or milmonavy macholi transplantation choice sequence (V) and milmonavy macholi transplantation choice sequence (V) and milmonavy macholi transplantation choice chock sequence (V) and milmonavy macholi transplantation choice chock sequence (V) and milmonavy macholi transplantation choice chock sequence (V) polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one The invention relates to a conjugate (I) comprising at least one nonprotein C sequence appearing as AAU99002 and the information in attached to

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Protein C zymogen protein mutant E309N/K311T
                                                                                                                                                                                                                                                                                                                                             sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99060 standard; protein;
                                                                                          Misc-difference
                                                                                                                           Misc-difference
                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVLLDSKKKCLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEVFVHPNYSKSTNDTDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                             309
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                           158.
                                                                                                                                                                                                                                      /labe1= Light_chain
                                                                           /note= "Wild-type Lys substituted by Thr"
                                                                                                           note= "Wild-type Glu substituted by Asn"
                                                                                                                                         label= Activation_peptide
                                                                                                                                                                         /label= Heavy_chain
                                                                                                                                                                                        'label= Lys_Arg_dipeptide
|58. 419
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Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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В Ş 뭉 S

61 13

121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180

SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVSFLNCSLDNGGCTHYCLLEVGWRRCSC 120

SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLBEVGWRRCSC 120

Matches 417; Conservative

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ANSFLEELKHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60

ANSFLEELRHSSLERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

Query Match

Local

Similarity

99.5**%**;

Score 2313; DB >; Pred. No. 1.6e-142; Pred. No. 1.6e-2;

Length 419; Indels

0;

Gaps

0

Sequence 419 AA;

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CC salte). Also included are (1) a variant (10) of (111) comprising of substitution in a position (2) where (3) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln, (2) are substitution is not Thr245Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln or Ph3315Ser/Ala/Thr/CC His/Lys/Arg/Asm/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (1V); (3) an expression vector (VI) comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC and in the manifacture of medicaments for the treatment (and CC diagnosis/prevention) of stroke, myocardial infarction, after venous (CC thrombosis, disseminated intravascular coagulation (DIC), sepsits, septic (2) shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow (CC transplantation, burns, pregnancy, major surgery/trauma or adult (2) recall clearance, reduced immunogenicity and/or increased resistance to activation by e.g. human plasma and alpha-1 ce increased serum half-life, increased resistant to inhibitors, reduced (2) cantitypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced (2) cantitypsin of less protein, and fewer side effects. Moreover, a conjugate offers a number of advantages over the currently available (2) cadministration of less protein, and fewer side effects. Moreover, a conjugate has an extended plasma life. The gene for protein C is conjugate has an extended plasma life. The gene for protein C is not conjugate and extended plasma life. The gene for protein C is not conjugate and should an extended plasma life. The gene for protein c is not conjugate and the infermation in claim 9 created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 created by the infermation in claim 9 created by the infermation in claim 9 created by the infermation in c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently
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18-OCT-2000; 2000US-024226BP.
21-UUN-2001; 2001DK-00000970.
21-UUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached ta protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pedersen AH, Freskgaard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; bulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
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Novel conjugate useful for treating or preventing septic shock, stroke
                                                                 WPI; 2002-489875/52.
                                                                                                                  Andersen KV,
                                                                                                                                                                                                                                                                 18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                                                                                                                                                                          MAXYGEN APS.
MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDXEAPQXSWAP 419
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                                                                                                                  Pedersen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Glu substituted by Asn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Wild-type Glu substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Activation_peptide/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                  Freskgaard
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and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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Claim 9; Page; 92pp; English.

polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 55% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Sequence 419 AA; The invention relates to a conjugate (I) comprising at least one non-

밁 5 Ş 밁 Ş 문 Ş 밁 8 Ş 밁 Matches 417; Query Match Local Similarity 301 241 241 181 181 121 121 61 61 1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120 GYHSSREKBAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACBGDS APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300 KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300 SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI Conservative 99.5%; 99.5%; Score 2313; DB 5; Pred. No. 1.6e-142 Mismatches .6e-142; Length 419; Indels 0, 180 240 360 180

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GYHSSRNKTAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS

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RESULT 95
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The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-0000970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                     Movel conjugate useful for treating or preventing septic shock, stroke and myccardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                 Andersen KV,
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                                                                                                                                                                                         Claim 9; Page; 92pp; English
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(MAXY-) MAXYGEN HOLDINGS LTD.
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158. .419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild-type Asp substituted by Ser"
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158. .169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Activation_peptide
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVFHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                        KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACNGSS
                                                                                                                                                                                                                                                               KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWBLDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEELRHSSLERECIBEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA
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Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 96

AAU99044 ID AAUS AAU99044 standard; protein; 419 AA

AAU99044;

XXXXXXX 23-AUG-2002 (first entry)

Human Protein C zymogen protein mutant L296N/T298S

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cc introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation cc site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least cc substitution is not inreased to the surface, with the proviso that the cubistitution is not inreased to the surface, with the proviso that the growpset/laf/mr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (Tyr30)25er/Alaf/mr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phals6Ser/Alaf/mr/CC (Tyr30)25er/Alaf/mr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phals6Ser/Alaf/mr/CC (Tyr); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC (I); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C) comprising (V); (4) a host cell (VII) (C) and in the manufacture of medicament for the functional in vivo half-CC (I); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C) and in the manufacture of medicaments for the treatment (and (C) diagnosis/prevention) of stroke, myocardial infarction, after venous (C) chock, emboli e.g. pulmonary emboli, transplantation (DIC), sepsis, septic chock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein ( has an intrapsed in vivo half-life, increased resistant to inhibitors, reduced cincreased serum half-life, increased resistant to inhibitors, reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide moiety (II) (e.g. an N-glycosyl group) covalently atta
a protein C polypeptide comprising an amino acid sequence which di
from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page; 92pp; English.
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MAXYGEN HOLDINGS LTD
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Matches 417; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC
                                                                                                                                                                                                 Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulati;
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               Peptide
                                                                                                                     Synthetic
                                                                                                                                           Homo sapiens
                                                                                                                                                                             adult respiratory distress syndrome; alpha-1 antitrypsin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPMVASFEGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIEGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYHSSREKEAKRURTFYLNFIKIPYVPHNECSEVMSNMYSENMLCAGILGDRQDACEGDS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                   /label= Light_chain
156. .157
                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2313; DB 5;
Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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/label= Lys\_Arg\_dipeptide

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comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
life or the serum half-life of a parent protein C polypeptide. The
conjugates, variants and protein C proteins are useful as medicaments,
and in the manufacture of medicaments for the treatment (and
diagnosis/prevention) of stroke, myocardial infarction, after venous
thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic
shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
transplantation, burns, pregnancy, major surgery/trauma or adult
respiratory distress syndrome (ARDS). The variant protein C has an
increased resistance to activation by e.g. human plasma and alpha-1
antitrypsin. The conjugates have an increased in vivo half-life,
increased serum half-life, increased resistant to inhibitors, reduced
                                                               increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available AFC products, including longer duration between injections, are duced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of AFC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
Sequence 419 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached ta protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen KV, Pedersen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Activation_peptide
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cell (VII)
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RESULT 98
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Matches 417;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
               15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                         sepsis, septic shock; embolism; purn; pregnancy; sepsis, septic shock; embolism; purn; pregnancy; sepsis, septic shock; embolism; purn; pregnancy; septis, septic shock; embolism; purnsary; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Protein C zymogen protein mutant T315N/V317S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2002
                                                                                                                              Misc-difference
                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                          bone marrow transplantation; major surgery; trauma; ARDS; adult respiratory distress syndrome; alpha-1 antitrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU99065 standard; protein; 419
                                                                               WO200232461-A2
                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWETLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KBVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPWQVVJLDSKKKLACGAVLIHPSWVJ.TAAHCMDESKKLJVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                               /note= "Wild-type Thr substituted by Asn" 317
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                             /label= Lys_Arg_dipeptide
L58. .419
                                                                                                              /note= "Wild-type Val substituted by Ser"
                                                                                                                                                                                                             /label=
                                                                                                                                                                              label=
                                                                                                                                                                                                                                                                           'label= Light_chain
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                                                                                                                                                                            Activation_peptide
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Pred. No. 1.6e-142;
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                                                                                                                                                                                                                                                                                                                                                                                               mutant; mutein.
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CC polypeptide moiety (II) (e.g. an Neglycosyl group) covalently attached to Co protein C polypeptide comprising an amino acid sequence which differs CC introduced and/or at least one removed amino acid sequence which differs CC site). Also included are (1) a variant (IV) of (III) in at least one cattachment group for the mon-polypeptide group (e.g. an N-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising an constitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not Th745Ser/ala/His/Iys/Arg/Ams/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Iys/Arg/Ams/Asp/Glu/Gly/Gln; (2) an uclpotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) CC comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The CC onjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and Cd diagnosis/prevention) of stroke, myocardial infarction, after venous comprisations (PC) because of serum half-life, increased in variant protein C polypeptide. The conjugates have an increased in vivo half-life, increased resistance to activation by e.g. human plasma and alpha-1 confirmation of less protein, and fewer side effects. Moreover, a caministration of less protein, and fewer side effects. Moreover, a caministration of less protein, and fewer side effects. Moreover, a caministration of less protein, and fewer side effects. Moreover, a calculation of less protein, and fewer side effects. Moreover, a calculation conjugate has an extended plasma life. The gene for protein C is calculated protein C is invention. Note: The gene for protein C is not the specification but was created by the indexer using the conjugate fination but was created by the indexer using the content of the invention.
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                                                                                          δ.
                                                                                                                              В
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                                                                                                                                                                                                 Matches 417;
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Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page; 92pp; English
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18-OCT-2000; 2000US-0242268P.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen KV,
                                                                                                                                                                                                                                                                                           protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAXY-) MAXYGEN APS
                                                                                                                                                                                                                Local
   121
                    121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                61
                                                                                               61
                                                                                                                                                                                                              Similarity
APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                              ANSFLEELRHSSLERECIEEICDFEBAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                      ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA 60
                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                             99.5%;
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                                                                                                                                                                                             0;
                                                                                                                                                                                                         Score 2313; DB 5;
Pred. No. 1.6e-142;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                              Length 419;
                                                                                                                                                                                             Indels
                                                                                                                                                                                             0.
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RESULT 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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                                                                                                                                                              18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                    25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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WPI; 2002-489875/52
                                               Andersen KV,
                                                                                                                                                                                                                                                                              15-OCT-2001; 2001WO-DK000679.
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                                                                                                               (MAXY-) MAXYGEN APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein C zymogen protein mutant V243N/V245T
                                                                                           MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRNFSLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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                                            Pedersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Val substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /labe1= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Wild-type Val substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       el= Lys_Arg_dipeptide
_419
                                            Æ,
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                                            Freskgaard PO
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

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361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein () conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as ANU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alphanantirpeased resistance to activation by e.g. human plasma and alphanantirpeased resistance to activation by e.g. human plasma and alphanantirpeased resistance to activation by e.g. human plasma and alphanantirpeased resistance to activation by e.g. human plasma and alphanantirpeased serum half-life, increased in vivo half life.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                           181
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SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFLEELRHSSLERECIEEI CDFBEAKEI FQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                             APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2313; DB 5;
Pred. No. 1.6e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 419;
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                      240
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RESULT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU99011;
                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Protein C zymogen protein mutant K192N/L194S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99011 standard; protein; 419
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                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                                                                    158.
                                                                                                                                                                                                                                                                                                                                                                                          /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Leu substituted by Ser'
                                                                                                                                                                                                                                                                                                                                                                                                             /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 2q13-q14;
                                                                                                                                                                                                                                                                                                                                                                         label= Activation_peptide/
                                                                                                                                                                                                                                                                                                                                                       note= "Wild-type Lys substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                     .419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stroke; myocardial infarction;
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18-OCT-2000; 18-OCT-2000; 21-JUN-2001; 21-JUN-2001; Andersen KV, Pedersen (-YXAM) MAXYGEN APS.
MAXYGEN HOLDINGS LTD ; 2000DK-00001560. ; 2000US-0242268P. ; 2001DK-00000970. ; 2001US-0300154P. AH, Freskgaard PO;

15-OCT-2001; 2001WO-DK000679

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2002-489875/52.

and myocardial infarction, Novel conjugate useful to protein a polypeptide for treating or preventing septic shock, stroke ion, comprises non-polypeptide group covalently polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

240

The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 55% of its side group exposed to the surface, with the proviso that the substitution is not thr/45ser/Ala/Hs/Ivs/Arg/Asn/Asp/Glu/Gly/Gln, Tyy302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or phe316Ser/Ala/Thr/Hi

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GGPMVASFHGTNFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419

GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS GYHSSREKEAKRURTEVI.NFIKIPVVPHNECSEVMSNMVSENMI.CAGII.GDRQDACEGDS KENFTHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI

360 300

301 301 241 241

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181

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after venous thrombosis; disseminated intravascular coagulation; DIC;

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AC AAU9
XX
AC AAU9
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DT 23-J
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DE Humm
KW Humm
KW Serv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 CC antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced CC increased serum half-life, increased resistant to inhibitors, reduced CC The conjugate offers a number of advantages over the currently available CC APC products, including longer duration between injections, caministration of less protein, and fewer side effects. Moreover, a CC conjugate anticoagulant activity is beneficial to reduce the risk of CC leeding while maintaining the antinflammatory activity of APC (activated protein C) conjugates. This must be especially important when CC conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not conducted protein confidence appearing as AAU99002 and the information in claim 9 cc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 417;
                                                                                                                                                                                                      AAU99023 standard; protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polyeptide. The conjugates, variants and protein C proteins are useful as medicaments,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis/prevention) of stroke, myocardial infarction, after venous
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                                                                                                                                                                                                                                                                                                                                                  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                 GYHS SREKEAKRNRTFVLNFTKI PVVPHNECSEVMSNMVS ENMLCAGILGDRODACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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Pred. No. 1.6e-142;
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serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; Human Protein C zymogen protein mutant K218N/L220S

23-AUG-2002

(first entry)

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The invention relates to a conjugate (I) comprising at least one non-
CC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
CC a protein C polypeptide comprising an amino acid sequence which differs
CC introduced and/or at least one removed amino acid sequence which differs
CC introduced and/or at least one removed amino acid sequence which differs
CC introduced and/or at least one removed amino acid sequence which differs
CC site). Also included are (I) a variant (IV) of (III) in at least one
CC substitution in a position (P) where (P) is an amino acid with at least
CC sto of its side group exposed to the surface, with the proviso that the
CC substitution is not Thr24SEx/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tiyr302Ser/Ala/Thx/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tiyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tigr302Ser/Ala/Thx/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tigr302Ser/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-489875/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-2001; 2001WO-DK000679
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The conjugate offers a number of advantages over the currently available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                    reduced immunogenicity and/or increased bioavailability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Light_chain
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RESULT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99084 standard; protein; 419 AA
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                                         Protein
                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  adult respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                  transplantation; major surgery; trauma; ARDS; ratory distress syndrome; alpha-1 antitrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C zymogen protein mutant R352N/D354T.
                                         /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                     /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%;
                                                                                                                   .157
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Pred. No. 1
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1.6e-142;
nes 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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/label= Heavy\_chain

Best Local Similarity

99.5%;

Score 2312; DB 5; Pred. No. 1.8e-142;

Length 419;

Query Match

Sequence 419 AA;

멼 Q 밁 Š 밁 V<sub>2</sub>

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Ct thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic chrombosis, disseminated intravascular coagulation (DIC), sepsis, septic cs shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow ctransplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an circulated resistance to activation by e.g. human plasma and alpha-1 cantitrypsin. The conjugates have an increased in vivo half-life, antitrypsin. The conjugates have an increased in vivo half-life, creased serum half-life, increased resistant to inhibitors, reduced crenal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available captured products, including longer duration between injections, cadministration of less protein, and fewer side effects. Moreover, a creduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antinflammatory activity of APC checking while maintaining the antinflammatory activity of APC the conjugate has an extended plasma life. The gene for protein C is created on chromosome 2gl3-gl4. The present sequence represents a zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc attachment group for the non-polypeptide group (e.g. an N-glycosylation cc site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CT Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe315Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-CC infe or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and diagnosis prevention) of stroke, myocardial infarction, after venous control of the procession in the procession in the control of the procession in the control of the procession control of the control of the control of the procession control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                       located on chromosome 2g13-g14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-489875/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200232461-A2
                                                        shown in the specification but was created by the indexer using protein C sequence appearing as AAU99002 and the information in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAXY-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Activation_peptide
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18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                             bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                      serum half-life; chromosome 2q13-q14; stroke; myocar after venous thrombosis; disseminated intravascular sepsis; septic shock; embolism; pulmonary embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein C zymogen protein mutant A310N/R312S
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                                         15-OCT-2001; 2001WO-DK000679
                                                                                                    WO200232461-A2
                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDNQTACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHSSREKEAKRNRIFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEVFVHPNYSKSTTDNDTALLHLAQPATLSQTTVPTCLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                        158.
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                          /note= "Wild-type Ala substituted by Asn"
                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                          /label= Light_chain
                                                                                                                             note= "Wild-type Arg substituted by Ser
                                                                                                                                                                                      /label= Activation_peptide
                                                                                                                                                                                                                 label= Heavy_chain
                                                                                                                                                                                                                               e1= Lys_Arg_dipeptide
_419
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                                                                                                                                                                                                        . 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                       stroke; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                         coagulation; DIC;
burn; pregnancy;
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PR 21-JUN-2001; 2001US-0300154P.

PR 21-JUN-2001; 2001US-0300154P.

PR (MAXY-) MAXYGEN APS.

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181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                          121 APGYKLGDDILQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                               417;
                                                                                                                               61 SLCCCHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                   61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                     1 ANSFLEEIRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                              APGYKLGDDILQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                      60
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Query Match

Local Similarity

99.5%;

Score 2312; DB 5; Pred. No. 1.8e-142;

Length 419;

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RESULT 104
ARU99046
ID AAU990
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                                                      Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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bone marrow transplantation; major surgery; trauma; ARDS;
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   Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                      WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-024226BP.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001WO-DK000679.
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                                                                                                                                                                                                                                                Pedersen AH, Freskgaard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Activation_peptide
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coagulant;
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ct attachment group for the non-polypeptide group (e.g. ann N-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC 15% of its side group exposed to the surface, with the proviso that the CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) excoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) (Comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-CC diagnosis/prevention) of stroke, myocardial infarction, after venous conjugates, variants and protein C proteins are useful as medicaments, CC diagnosis/prevention) of stroke, myocardial infarction, after venous ctransplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an CC increased resistance to activation by e.g. human plasma and alpha-1 conjugate offers a number of advantages over the currently available CC The conjugate offers a number of advantages over the currently available CC C moducts. including longer duration between injections.
                                                                                                                                                                                                                                                                                                                                         APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                       located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
Sequence 419 AA;
                                                                                                             protein C sequence appearing as AAU99002 and the information in claim 9
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S 밁 Ş 멍 Ś S 먉 S 밁 8 먉 Š Matches 417; Query Match Best Local : 181 181 121 121 301 301 241 61 61 <u>, , </u> Similarity ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419 GGPMVASEHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKRAPQKSWAP KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA GNHTSREKEAKRNRT FYLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS KEVFVHPNYSKSTIDNDIALLHLAQPAILSQTIVPICLPDSGLAERELNQAGQETLVTGW APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD Conservative 99.5%; <u>,</u> Score 2312; DB 5; Pred. No 1.8e-142; Mismatches Length 419; Indels 0; Gaps 419 360 360 240 240 180 120 120 60

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The invention relates to a conjugate (I) comprising at least one non-cc polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs cf from that of a parent protein C polypeptide (III) in at least one controlled that of a parent protein C polypeptide (III) in at least one controlled and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation csite). Also included are (I) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least csite). Also included are to the surface, with the provise that the substitution is not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln (Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) (C) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersen KV,
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MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2913-914. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   renal clearance, reduced immunogenicity and/or increased bioavailability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                             GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                     KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVFICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                  SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANSFLEELRHSSLERECIEBICDFEBAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                  GYHSSREKENKTNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                     SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWEKWELDLDI
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RESULT 106
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AAU99038 AAU99038 standard; protein; 419 AA

AAU99038

23-AUG-2002 (first entry)

Human Protein C zymogen protein mutant T253N/D255T.

**EEEEEEEEE** Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;

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The conjugate offers a number of APC products, including longer of administration of less protein,
                                      diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available ARC products, including longer duration between injections, administration of learnership and femeration between injections.
                                                                                                                                                                                                                                                                                                                                                                        25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-life or the serum half-life of a parent protein C polyaperide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and are useful) of the transfer of medicaments for the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment of the treatment 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen KV, Pedersen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2001;
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2001US-0300154P.
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HOLDINGS LTD
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                                                                                                                                      Key
                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                        bone marrow transplantation; major surgery; trauma; ARDS; coagulant; muadult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mu
                                                                                                                                                                                                                                                         Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
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                  Peptide
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                                                                                                                                                                                                                                                                                                                                               Protein C zymogen protein mutant G383N/G385S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                  /label= Light_chain
                                                                                                                                      Location/Qualifiers
                                    /label=
                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%;
                                                 eı= Lys_Arg_dipeptide
_419
                    .169
Activation_peptide
                                Heavy_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2312; DB 5;
Pred. No. 1.8e-142;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                C; zymogen;
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                                                                                                                                                                                                                                                                                 DIC;
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attachment group for the non-polypeptide group (e.g. an M.-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not Thr24SSer/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe3i6Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe3i6Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-CC infe or the serum half-life of a parent protein C polypeptide. The CC comjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and CC diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic Shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow crespiratory distress syndrome (ARDS). The variant protein C has an CC increased resistance to activation by e.g. human plasma and alpha-1 concreased sestime to activation by e.g. human plasma and alpha-1 concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to inhibitors, reduced concreased serum half-life, increased resistant to combine to concreased concreased resistant to manufacture.
     Matches 417; Conservative
                                Best Local Similarity
                                                   Query Match
                                                                                                                                                                           increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to creduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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18-OCT-2000; 2000US-0242268P.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
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                                                                                                          Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2002
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                                                                                                                                                        protein {	t C} sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAXYGEN HOLDINGS LTD
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                        99.5%;
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  0;
Score 2312; DB 5;
Pred. No. 1.8e-142;
0; Mismatches 2;
                                                   Length 419;
     Indels
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   RESULT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU99086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99086 standard; protein; 419 AA
18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Protein C zymogen protein mutant E357N/D359T.
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                                                                                       15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GGPMVASFHGTWFLVGLVSWGENCSLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GGPMVASFHGTWELVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                359
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                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                            note= "Wild-type Asp substituted by Thr"
                                                                                                                                                                                                                                                                                                label= Heavy_chain
                                                                                                                                                                                                                                                                                                                               /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                  /label= Light_chain
                                                                                                                                                                                                                              note= "Wild-type Glu substituted by Asn"
                                                                                                                                                                                                                                                             label= Activation_peptide
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crespiratory distress syndrome (ARDS). The variant protein C has an
increased resistance to activation by e.g. human plasma and alpha-1
created increased resistance to activation by e.g. human plasma and alpha-1
created serum half-life, increased resistant to inhibitors, reduced
crenal clearance, reduced immunogenicity and/or increased bioavailability.
Created the conjugate offers a number of advantages over the currently available
created products, including longer duration between injections,
cadministration of less protein, and fewer side effects. Moreover, a
creduced anticoagulant activity is beneficial to reduce the risk of
creduced anticoagulant activity is beneficial to reduce the risk of
cleading while maintaining the antiinflammatory activity of APC
cleated protein C) conjugates. This must be especially important when
the conjugate has an extended plasma life. The gene for protein C is
considered in chromosome 3013-014 plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypoptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached t a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (I) a variant (IV) of (III) comprising a site). Also included are (I) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page; 92pp;
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                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGBYDLRRWEKWELDLDI
                                                           SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                            SICCGHGTCIDGIGSFSCDCRSGWEGRFCQRBVSFINCSIDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                   ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2312; DB 5;
Pred. No. 1.8e-142;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 419;
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RESULT 109
AAU99091
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18-OCT-2000; 2000US-024226BP
21-JUN-2001; 2001DK-00000970
                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                  21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Protein C zymogen protein mutant L387N/N389S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU99091 standard;
                                                                                                                                                                                                                                             15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                       25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oone marrow
                                                                                                                       Andersen
                                                                                                                                               (-YXXM)
                                                                                                                                                                                                                                                                                              NO200232461-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              narrow transplantation; major surgery; trauma; ARDS; coagulant; respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                               MAXYGEN HOLDINGS LTD
                                                                                                                                                          MAXYGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACNGTS
                                                                                                                      ζ,
                                                                                                                                                                                  2001US-0300154P
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                                                                                                                       Pedersen
                                                                                                                                                                                                                                                                                                                                  389
                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Asn substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                           /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                    'label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                             note= "Wild-type Leu substituted by Asn"
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                                                                                                                       AH,
                                                                                                                      Freskgaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           harn; pregnancy; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

WPI; 2002-489875/52.

The invention relates to a conjugate (I)

comprising at least one non-

Claim 9; Page; 92pp; English.

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Combititution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the provise that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (VI); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (5) increasing (VI); (6) increasing (VI); (6) increasing (VI); (7) increasing (VI); (7) increased (VI); (7) increased (VI); (8) increased (VI); (8) increased (VI); (8) increased (VI); (8) increased (VI); (8) increased (VI); (8) increased (VI); (8) increased (VI); (8) increased (VI); (8) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein C sequence appearing as AAU99002 and the information in claim 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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GGPMVASFHGTWFLVGLVSWGEGCGLNHSYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                        GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 1.8e-142;
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serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation, DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; mutein.
                                                                                                                                                                                                                                                                                               18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Protein C zymogen protein mutant D255N/D257T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU99042 standard; protein; 419 AA.
                                                                                                                                                                                                                                                                                                                                                 15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                   (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Asp substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy_chain
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Andersen KV,

Pedersen AH, Freskgaard PO,

WPI; 2002-489875/52.

Claim 9; Page; 92pp; English

The invention relates to a conjugate (I) comprising at least one non-compressing and protein C polypeptide molety (II) (e.g. an N-glycosy) group) covalently attached to CC a protein C polypeptide comprising an amino acid sequence which differs CC from that of a parent protein C polypeptide (III) in at least one attachment group for the non-polypeptide group (e.g. an N-glycosylation cathering and compressing an attachment group for the non-polypeptide group (e.g. an N-glycosylation CC site), Also included are (1) a variant (IV) of (III) comprising a compatition of the side group exposed to the surface, with the proviso that the compressing and CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a mucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) CC comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-CC life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bloavailability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1
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                                                                                                          serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                            sepsis; septic shock; embolism; pulmonary embolism;
                                                                                                                                                                               Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                       Human Protein C zymogen protein mutant L220N/R222T
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Pred. No. 1.8e
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coagulant;
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18-OCT-2000;
18-OCT-2000;
21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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WPI; 2002-489875/52
                                                                                                             21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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                              Andersen
                                                                                                                                                                                         15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                              MAXYGEN HOLDINGS LTD
                                                                               MAXYGEN APS
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                                                                                                             ; 2000US-0242268P.
; 2001DK-00000970.
; 2001US-0300154P.
                                                                                                                                                          2000DK-00001560
                              Pedersen AH,
                                                                                                                                                                                                                                                                                                                                                                      158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Light_chain
                                                                                                                                                                                                                                                                                   /note= "Wild-type Arg substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                              /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                     note= "Wild-type Leu substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                     'label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                  label= Heavy_chain
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                              Freskgaard PO;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English

CC polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to Colypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to C a protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid sequence which differs CC introduced and/or at least one removed amino acid residue comprising an CC site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC 25% of its side group exposed to the surface, with the proviso that the CC 17%1025ex/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a mucleotide sequence (V) encoding (CIV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (V2) the functional in vivo half-CC infe or the serum half-life of a parent protein C polypeptide. The CC comprising (V) or (VI); (5) increasing (V2) the functional in vivo half-CC and in the manufacture of medicaments for the treatment (and C diagnosis/prevention) of stroke, myocardial infarction, after venous CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increasing resistance to activation by a minam with amain and alpha-1 increased resistance to activation by a minam and alpha-1 administration of less protein, and fewer side effects. Moreover, reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced imminogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available appropriately. Including longer duration between injections. The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attache

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                                           Misc-difference
                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Protein C zymogen protein mutant V243N/V245S.
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                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sepsis; septic shock; embolism; pulmonary embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLNVTLGEYDLRRWEKWELDLDI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
/note= "Wild-type Val substituted by Asn'
                                                                                                                        /label= Heavy_chain
                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                              /label= Light_chain
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                   label= Activation_peptide
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99.5%;
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                                                                                                                                                                                                                                .157
                                                                                                                                                                                               Lys_Arg_dipeptide
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Pred. No. 2.1e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 

Best Local Similarity Matches 417; Conserv

Conservative

0; Mismatches Score 2311; Pred. No. 2.

2.1e-142; nes 2; DB 5;

0; Gaps

50

Length 419; Indels

99.4%;

Query Match

Sequence 419 AA;

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cc polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to ca protein C polypeptide comprising an amino acid sequence which differs cfrom that of a parent protein C polypeptide (III) in at least one can that of a parent protein C polypeptide (III) in at least one can troduced and/or at least one removed amino acid residue comprising an catachment group for the non-polypeptide group (e.g. an N-glycosylation cities). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least comparent comprision and comprision of the sufface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, cry302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/A
                                              renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, prespancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors, reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a conjugate (I) comprising at least one non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attached to protein C polypeptide comprising an attachment group.
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(MAXY-) MAXYGEN HOLDINGS LTD.
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                             18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                               Peptide
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 (MAXY-) MAXYGEN APS
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                                                                                                   15-OCT-2001; 2001WO-DK000679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KENFSHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVILLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKENEKKRSHLKRDTEDQEDQVDPRLIDGKNTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSIDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                     222
                                                                                                                                                                                                                                  220
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                    note= "Wild-type Arg substituted by Ser"
                                                                                                                                                                                                                                             /label= Activation_peptide
                                                                                                                                                                                                                                                                          /label= Heavy_chain
                                                                                                                                                                                                                                                                                                      /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                       /label= Light_chain
156. .157
                                                                                                                                                                                                                 note= "Wild-type Leu substituted by Asn"
                                                                                                                                                                                                                                                               . 169
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Andersen KV, Pedersen AH, Freskgaard
                                                              (MAXY-) MAXYGEN HOLDINGS LTD
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WPI; 2002-489875/52

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

The invention relates to a conjugate (I) comprising at least one nonCC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
CC a protein C polypeptide comprising an amino acid sequence which differs
CC from that of a parent protein C polypeptide (III) in at least one
CC introduced and/or at least one removed amino acid residue comprising an
CC attachment group for the non-polypeptide group (e.g. an N-glycosylation
CC site). Also included are (I) a variant (IV) of (III) comprising a
CC substitution in a position (P) where (P) is an amino acid with at least
CC 5% of its side group exposed to the surface, with the proviso that the
CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
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CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/G cc increased serum half-life, increased resistant to inhibitors, reduced crenal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available captures including longer duration between injections, captures, and fewer side effects. Moreover, a creduced anticoagulant activity is beneficial to reduce the risk of certification of less protein, and fewer side effects. Moreover, a creduced anticoagulant activity is beneficial to reduce the risk of certification protein conjugates. This must be especially important when certificated protein C) conjugates. This must be especially important when certificated on chromosome 2g13-g14. The present sequence represents a zymogen conjugate has an extended plasma life. The gene for protein C is cated on chromosome 2g13-g14. The present sequence is not constant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the corporation C sequence appearing as AAU99002 and the information in claim 9 shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-l antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors. Sequence 419 AA;

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                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLNVSLGEYDLRRWEKWELDLDI
                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                        99.4%;
99.5%;
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                        Score 2311;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                      .1e-142;
                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                           Indels
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KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated infravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                        Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                           18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein C zymogen protein mutant L349N/D351S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU99079 standard; protein; 419 AA
                                                                                                                                  WPI; 2002-489875/52.
                                                                                                                                                            Andersen KV,
                                                                                                                                                                                                                                                                                             15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                                                                                                                  WO200232461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult respiratory distress syndrome; alpha-l antitrypsin; mutant; mutein.
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                                                                                                                                                                                     MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                   MAXYGEN APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYHSSREKEAKRNRTFVLNFIKIÞVVÞHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPMVASFHCTWFLVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                           Pedersen AH,
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158. .419
//_ar.
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156. 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       note= "Wild-type Asp substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Leu substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= Heavy_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow of transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 concincreased serum half-life, increased are stant to inhibitors, reduced increased serum half-life, increased resistant to inhibitors, reduced concincreased serum half-life, increased resistant to inhibitors, reduced concincreased serum half-life, increased versitant to inhibitors, reduced concincreased serum half-life, increased versitant to inhibitors, reduced concincreased protein of less protein, and fewer side effects. Moreover, a standard products, including longer duration between injections, committation of less protein, and fewer side effects. Moreover, a concincreased protein of less protein, and fewer side effects. Moreover, a conjugate maintaining the antiinflammatory activity of APC (activated protein C onjugates, This must be especially important when the conjugate has an extended plasma life. The gene for protein C is coated on chromosome 2q13-q14. The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 or the conjugate appearing as AAU99002 and the information in claim 9 or the conjugate protein of the specification but was created by the information in claim 9 or the conjugate protein of the specification but was created by the information in claim 9 or the conjugate protein conjugate has an extended plasma life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from that of a parent protein C polypeptide (III) in at least one cintroduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation comprising a position of the non-polypeptide group (e.g. an N-glycosylation comprising a substitution in a position (P) where (P) is an amino acid with at least comprisition of the group exposed to the surface, with the proviso that the substitution is not Thr485ser/Ala/Hai/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-comprising (V) and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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                                        GGPMVAS FHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                       GYHSSREKEAKRNRTFVLNFIKIFVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                  KEVFVHDNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                          SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                              GYHSSREKEAKRNRTFVLNF1K1PVVPHNECSEVMSNMVSENMLCAGINGSRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 2311; DB 5; 99.5%; Pred. No. 2.1e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 419;
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The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs

Claim 9; Page; 92pp; English

AAU99077 AAU99077 standard; protein; 419 AA

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The invention relates to a conjugate (I) comprising at least one non-
CC polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to
CR a protein C polypeptide comprising an amino acid sequence which differs
CR from that of a parent protein C polypeptide (III) in at least one
CR introduced and/or at least one removed amino acid residue comprising an
CR site). Also included are (I) a variant (IV) of (III) comprising a
CR substitution in a position (P) where (P) is an amino acid with at least
CR substitution is not Thr24SSer/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CR TY302Ser/Ala/Thr/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CR His/Lys/Arg/Asm/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding
CR His/Lys/Arg/Asm/Asp/Glu/Gly/Gln; (3) an expression vector (VI) comprising (V); (4) a host cell (VII)
CR comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
CR iffe or the serum half-life of a parent protein C polypeptide. The
CR conjugates, variants and protein C proteins are useful as medicaments,
CR diagnosis/prevention) of stroke, myocardial infarction, after venous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                    Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sepsis; septic shock; embolism; pulmonary embolism; burn; bone marrow transplantation; major surgery; trauma; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU99077;
                                                                                                                                                                                                                                                                                                                                      Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-489875/52.
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18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Wild-type Gly substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label=
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reductions and the conjugates have a resistant to inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein C sequence appearing as AAU99002 and the information in claim 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis, disseminated intravascular coagulation (DIC),
361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                              GGPNVASFHGTWEIVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGNLSDRQDACEGDS
                                                                                                                    GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                               SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 AA;
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                    KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 burns, pregnancy, major surgery/trauma or adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%;
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Pred. No. 2
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ches 2;
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RESULT 116
 23-AUG-2002
                                                                         AAU99092 standard; protein; 419 AA.
(first entry)
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Human Protein C zymogen protein mutant L387N/N389T

serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; mutaint; mutein. Homo sapiens Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;

Peptide Protein Peptide

Protein

Length 419; Indels

0;

Gaps

240

240 180 120

60

360

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cc attachment group for the non-phypeptide group (e.g. an N-phycosylation cosite). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the comprisition is not fhr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln.

CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln (2) a nucleotide sequence (V) encoding CC (TV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (2) an expression vector (VI) comprising (V); (4) a host cell (VII) (2) comprising (V) or (VI); (5) increasing (W) the functional in vivo half-cc (11fe or the serum half-life of a parent protein C polypeptide. The CC conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and cdiagnosis/prevention) of stroke, myocardial infarction, after venous cc thromboeis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow crassplantation, burns, pregnancy, major surgery/trauma or adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                             respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced remai clearance, reduced immunogenicity and/or increased bloavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001WO-DK000679
                            reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide moiety (II) (e.g. an N-glycosyl group) covalently att. a protein C polypeptide comprising an amino acid sequence which d from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen KV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
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   conjugate has an extended plasma life.
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156. .157
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The gene for protein C is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein C_i intravascular coagulation; deep vein thrombosis; pulmonary embolism; protein C deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR 62653;
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                            Region
                                                                                    Region
                                                                                                                                                                                                                                                                                                                           Region
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27-JUN-1995
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                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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Local Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGYKLGDDLLQCHPAVKFPCGRPWKKMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYHS SREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                       /note= "pre-pro peptide"
43. .211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
/label= glycosylation_site
                                                        /label= glycosylation_site
                                                                                                                /label= glycosylation_site
                                                                                                                                                                               note=
                                                                                                                                                                                                                                    note= "corresponding codon ACC"
                                                                                                                                                                                                                                                                                            /label= glycosylation_site
                                                                                                                                                                                                              . 46
                                                                                                                                                                        "activated protein C heavy chain"
                                                                                                                                                                                                                                                                                                                                                       "activation peptide"
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Pred. No. 2.1e-142;
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Human Protein C zymogen protein mutant G383N/G385T

,880990BB

23-AUG-2002

(first entry)

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Best Local
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27-APR-1990;
27-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intravascular coagulation, e.g. deep vein thrombosis and pulmonary embolism. They may also be used in the treatment of inherited protein C deficiency. The modified protein C has the advantage of increased stability in plasma and thus a greater half-life compared to prepns. of human protein C purified from plasma. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ72994 encodes AAR62653 human protein C, from which the modified protein C molecule described in AAR62654 is derived. The modified molecule is useful in the treatment of a variety of conditions involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified human protein C molecules - esp. useful for treating coagulation -related disorders such as Protein C deficiency or thrombosis, or for promoting fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 461 AA;
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                      GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                               GYHSSREKEAKRNRTFVLNFÍKÍ ÞVVÞHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                               KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                       KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLYTGW
                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGTPWKGMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                            APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                             SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                       SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                             ANSFLEELRHSSLERECIEETCDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foster DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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90US-00515378.
90US-00634988.
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Pred. No. 2.3e-142; ...
Pred. no. 2.3e-142; ...
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
                                                                                                                                                                   18-OCT-2000; 2000DK-00001560
18-OCT-2000; 2000US-0242268P
21-JUN-2001; 2001UK-00000970
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WPI; 2002-489875/52
                                          Andersen
                                                                                                                                                     21-JUN-2001; 2001US-0300154P
                                                                                                                                                                                                                                                                   15-OCT-2001; 2001WO-DK000679
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                                                                                                             (MAXY-)
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                                                                                    MAXYGEN APS.
MAXYGEN HOLDINGS LTD
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                                          Pedersen
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                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Gly substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Light_chain
156. .157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *1= Lys_Arg_dipeptide
                                          AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Wild-type Gly substituted by Asn"
                                          Freskgaard PO;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

The invention relates to a conjugate (I) comprising at least one nonCC polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
CC a protein C polypeptide comprising an amino acid sequence which differs
CC from that of a parent protein C polypeptide (III) in at least one
CC introduced and/or at least one removed amino acid residue comprising an
CC stab. Also included are (I) a variant (IV) of (III) comprising a
CC substitution in a position (P) where (P) is an amino acid with at least
CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln,
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
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CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/G

RESULT 118
AAU99088
ID AAU990
XX

AAU99088 standard; protein; 419 AA

Misc-difference

/label= Activation\_peptide

Peptide

Peptide

/label=

Lys\_Arg\_dipeptide Heavy\_chain

/label=

.169 .419 Protein

Location/Qualifiers

/label= Light\_chain

.157

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RESTLT 119
AAU9908
ID AAU990
AC AAU990
AC AAU990
XX Z3-AUG
XX Human
XX Human
XX Human
XX Human
XW serum
KW serum
KW serum
KW sepois
KW bone m
KW bone m
KW JX X
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 417; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced remaind clearance, reduced immunogenicity and/or increased bioavailability.
                                                                                                                                                                          Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU99068 standard;
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                                                                                                                 sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                            Human Protein C zymogen protein mutant F316N/L318T
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                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 419
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Pred. No. 2.5e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                      antitrypsin; mutant; mutein.
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Synthetic

Homo sapiens

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CC introduced and/or at least one removed amino acid residue comprising an CC attachment group for the non-polypeptide group (e.g. an W-glycosylation CC site). Also included are (1) a variant (IV) of (III) comprising a CC substitution in a position (P) where (P) is an amino acid with at least CC 25% of its side group exposed to the surface, with the proviso that the CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln.

CC Ty302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/
CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII)
CC comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-
CC life or the serum half-life of a parent protein C polypeptide. The CC onjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and C diagnosis/prevention) of stroke, myocardial infarction, after venous CC thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic CC shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow CC transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ABDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available of the conjugate offers a number of advantages over the currently available.
                  APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a conjugate (I) comprising at least one non-
polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attache
a protein C polypeptide comprising an amino acid sequence which diffe
from that of a parent protein C polypeptide (III) in at least one
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18-OCT-2000; 2000US-024226BP.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 318
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(MAXY-) MAXYGEN HOLDINGS LTD.
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located on chromosome 2 \mathtt{q} 13 	ext{-} \mathtt{q} 14 . The present sequence represents a zymogen
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XX Human;
KW Serum
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Best Local :
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                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                             Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
                                         Misc-difference 35]
                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protein C zymogen protein mutant L349N/D351T
                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                  Homo sapiens
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bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
              /note= "Wild-type Asp substituted by Thr"
                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                      'label≃
                                                                                                                                                                                                            /label= Light_chain
                                                   note= "Wild-type Leu substituted by Asn"
                                                                                               abel=
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99.5%;
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                                                                                             Activation_peptide
                                                                                                                                  Heavy_chain
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Pred. No. 2.5e-142;
Prematches 2;
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61

SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120

ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA

Query Match Best Local S Matches

Local Similarity 417;

99.4%;

Score 2310; Pred. No. 2. Mismatches

2.5e-142; ches 2;

0

Gaps

60

DB 5;

Length 419; Indels

Conservative

0

Sequence 419 AA;

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increased resistance to activation by e.g. human plasma and alpha-1 (C antirrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased in vivo half-life, c increased serum half-life, increased in vivo half-life, c increased in vivo half-life, increased serum half-life, increased in vivo half-life, c increased serum half-life, increased in vivo half-life, increased serum half-life, increased in vivo half-life, c increased serum half-life, increased bioavailability. The conjugate offers a number of advantages over the currently available c APC products, including longer duration between injections, c administration of less protein, and fewer side effects. Moreover, a creduced anticoagulant activity is beneficial to reduce the risk of c leeding while maintaining the antiinflammatory activity of APC c activated protein C onjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is coated on chromosome 2q13-q14. The present sequence is not c located on chromosome 2q13-q14. The present sequence is not c shown in the specification but was created by the indexer using the c protein C sequence appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate appearing as AAU99002 and the information in claim 9 to the conjugate protein conjugate and the conjugate protein conjugate appearing the conjugate 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln, Cryr302Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln, Cryr302Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln; Cryr302Ser/Ala/His/Lys/Arg/Asm/Asp/Glu/Gly/Gln; Cryr302Ser/Ala/His/Crys/Arg/Asm/Asp/Glu/Gly/Gln; Cryr302Ser/Ala/His/Crys/Arg/Asm/Asp/Glu/Gly/Gln; Cryr302Ser/Ala/His/Crys/Arg/Asm/Asp/Glu/Gly/Gln; Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/Cryr302Ser/Ala/His/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200232461-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-489875/52.
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Protein C Zymogen FLIN comprises a signal peptide and propeptide of a gamma-carboxylated secreted protein, the light chain of HPC, a basic dipeptide (i.e. Lys-Arg, but can also be Arg-Lys, Lys-Lys or Arg-Arg) and amino acid residues 200-461 of HPC but with Asp(209) replaced by Phe and Asp(214) replaced by Asn. The zymogen can be activated in vivo by thrombin alone (even in the presence of calcium) and is more susceptible to activation by thrombin, thrombomodulin than native HPC zymogen. Zymogen FLIN can be administered as a pro drug useful in prevention and treatment of diseases involving intravascular coagulation. It can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPC mutant; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-2003
31-OCT-1991
                                                                                                                                                                                                                                                         Recombinant mutants of human protein increased sensitivity to activation thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR13540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13540 standard; protein; 461
                                                                                                                                                                                                               Claim 28; Page 37-38; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                            1991-254444/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVVTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGINGTRODACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERBLNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCNDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                      Grinnell BW;
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-00484133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91EP-00301450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug; intravascular coagulation; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Lys-Arg dipeptide
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by thrombin
                                                                                                                                                                                                                                                                             aminoacid changes for and thrombin-
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            given to thrombocytopenic patients with invasive cancers with and intensive chemotherapy. See also ARR13537-9 and ARR13623. 09-UAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 461 AA;
                   /note= "Wild-type Val substituted by Asn" Misc-difference 247
                                                                                                                                                                                                                                                                                                                                                                                    serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU99029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU99029 standard; protein; 419
                                                                                                                                                       Protein
                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Protein C; N-glycosylation; APC; activated protein C; zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Protein C zymogen protein mutant V245N/P247S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mutein.
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/label=
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        /note= "Wild-type Pro substituted by Ser"
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                                                                                       Activation_peptide
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Best Local :
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18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
                                                                                                                                                            Sequence 419 AA;
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ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA 60
                           ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLDLEHPCA
                                                                             Conservative
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99.5%;
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Pred. No. 2.9e
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21-JUN-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                 Key
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                                                    ; 2000DX-00001560.
; 2000US-0242268P.
; 2001DK-00000970.
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158. .419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, and interest administration of less protein, and fewer side effects. Moreover, and interest and include the risk of reduced anticoagulant activity is beneficial to reduce the risk of reduced anticoagulant activity is beneficial to reduce the risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased resistant to inhibitors, reduce increased serum half-life, increased resistant to inhibitors, reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a conjugate (I) comprising at least one non-
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                               KEVFVHPNYSKSTTDNDIÄLLHLAQPÄTLSQTIVPICLPDSGLÄERELNQAGQETLVTGW 300
                                                                                                                                          SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                           SICCGHGTCIDGIGSESCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEBICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA
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99.5%;
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Pred. No. 2.9e-142;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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            The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one
                                                                                                                                                                                                                                                                               18-OCT-2000; 2000DK-00001560.
18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
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                                                                                     Claim 9; Page;
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                                                                                                                                                                                                         Andersen KV,
                                                                                                                                                                                                                                       (MAXY-)
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MAXYGEN HOLDINGS LTD
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introduced and/or at least one removed amino acid residue

comprising an

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CC 25% of its side group exposed to the surface, with the proviso that the consistitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (TV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) CC comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-clife of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and clasgosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, embodi e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alphalic antitrypsin. The conjugates have an increased in vivo half-life, cantitrypsin. The conjugates have an increased in vivo half-life. The conjugates have an increased in vivo half-life antitrypsin. The conjugates have an increased in vivo half-life. Cantitrypsin. The conjugates have an increased in conjugate offers a number of advantages over the currently available candinistration of less protein, and fewer side effects. Moreover, a conjugate protein C has an activity is beneficial to reduce the risk of the conjugate plasma life. The cense for wortein C is cativated protein C) conjugates. This must be especially important when conjugate has an attended national field in the conjugate servence and the conjugate offers and the conjugate offers and the conjugate offers and the conjugate offers and the conjugate offers and the conjugate offers and the conjugate offers and the conjugate offers and the conjugate of the conjugate of a parameter of the conjugate of the conjugate of the conjugate of the conjugate of the conjugate of the conjugate of the conjugat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGYKLGDDLLQCHPAVKPPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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a position (P) where (P) is an amino acid with at least
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Pred. No. 2.9e-142;
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC;
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                                                                                                                                 18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                                      (MAXY-) MAXYGEN HOLDINGS LTD
                                                                                   (MAXY-) MAXYGEN APS
Pedersen AH, Freskgaard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Leu substituted by Ser"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Wild-type Phe substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Heavy_chain
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coagulant;
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Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

Claim 9; Page; 92pp; English.

substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Thr245Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least polypeptide molety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an The invention relates to a conjugate (I) comprising at least one non-

RESULT 125
AAU99067
ID AAU990

AAU99067 standard; protein; 419 AA

AAU99067

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ARESULT 126
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on Chromosome 2913-914. The present sequence represents a zymogen protein C arriant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as ANU99002 and the information in claim 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-l antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 419 AA;
                         Homo sapiens
Synthetic.
                                                                                          Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intraccular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin; mutant; mut
                                                                                                                                                                                                                                                                    Human Protein C zymogen protein mutant H388N/Y390S
                                                                                                                                                                                                                                                                                                                       23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    AAU99093 standard; protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPMVASEHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYHSSREKEAKRNRTNVSNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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Pred. No. 2.9e-142;
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CC polypeptide moiety [II] (e.g. an N-glycosyl group) covalently attrached to polypeptide moiety [II] (e.g. an N-glycosyl group) covalently attrached to CC a protein C polypeptide comprising an amino acid sequence which differs C from that of a parent protein C polypeptide (III) in at least one controduced and/or at least one removed amino acid residue comprising an extrachment group for the non-polypeptide group (e.g. an N-glycosylation C site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, CC Tyr30ZSer/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding CC (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) C comprising (V) or (VII); (5) increasing (M2) the functional in vivo half-CC conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
CC diagnosis/prevention) of stroke, myocardial infarction, after venous consists of the control of stroke, myocardial infarction (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow cransplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alphalic antirypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced cransplantation offers a number of advantages over the currently available care products, including longer duration between injections, and creduced anticoagulant activity is beneficial to reduce the risk of the ding while maintaining the antiinflammatory activity of APC bleeding while maintaining the antiinflammatory activity important when conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen control of the invention. Note: The present sequence is not
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18-OCT-2000;
21-JUN-2001;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
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(MAXY-) MAXYGEN HOLDINGS LTD
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2001US-0300154P
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2000US-0242268P.
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ARBSULT 127
AAU3900 127
AAU3900 XX
AC AAU990 XX
AC AAU990 XX
AC AAU990 XX
BY Human 123 - AUG
XX Human 123 - AUG
XX Human 123 - AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Protein C zymogen protein mutant H388N/Y390T
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adult respiratory distress syndrome; alpha-1 antitrypsin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APGYKLGDDILQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                                                                                                                                                                                                                                            /label= Lys_Arg_dipeptide
158. .419
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               /label= Light_chain
                                                          note= "Wild-type Tyr substituted by Thr"
                                                                                                                                                                                                                                           /label= Heavy_chain
                                                                                                                    note= "Wild-type His substituted by Asn"
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                                                                                                                                                                                                                                                                                                                                         .157
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5 B 5

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SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120

Query Match Best Local : Matches 41

Local Similarity

99.3%;

Score 2308; D Pred. No. 3.3e 1; Mismatches

)8; DB 5; 3.3e-142;

Length 419; Indels

0

Gaps

60

Conservative

Sequence 419 AA;

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XX IS-OCT-2001; 2001WO-DK000679.

XX IS-OCT-2001; 2001WS-DK0005560.

RX IS-OCT-2000; 2000WS-00001560.

RX IS-OCT-2000; 2000WS-00001560.

RX IS-OCT-2000; 2000WS-00001560.

RX IS-OCT-2000; 2000WS-00001560.

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              Andersen KV,
                                                                                 18-CCT-2000; 2000DK-00001560.

18-CCT-2000; 2000US-0242268P.

21-JUN-2001; 2001DK-00000970.

21-JUN-2001; 2001US-0300154P.
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                                         (MAXY-) MAXYGEN APS.

(MAXY-) MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEPMVAS FHGTWFLVGLVSWGEGCGLLNNTGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYHSSREKEAKRNRTFYLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
              Pedersen AH,
                                                                                                                                                                                                                                                    /note= "Wild-type Leu substituted by Asn"
388
                                                                                                                                                                                                                                       /note= "Wild-type His substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                  /label= Light_chain
156. .157
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                              label= Activation_peptide
                                                                                                                                                                                                                                                                                                                                       e1= Lys_Arg_dipeptide
.419
             Freskgaard PO;
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WPI; 2002-489875/52

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

CC polypoptide molety (II) (e.g. an N-glycosyl group) covalently attached to CC a protein C polypoptide comprising an amino acid sequence which differs C from that of a parent protein C polypoptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an CC attachment group for the non-polypoptide (III) comprising a N-glycosylation C site). Also included are (1) a variant (IV) of (III) comprising a least trution in a position (P) where (P) is an amino acid with at least CC substitution in a position (P) where (P) is an amino acid with at least CC substitution is not fhr24Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, (Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or PhealiSer/Ala/Thr/CC Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or PhealiSer/Ala/Thr/CC His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding C (IV); (3) an expression vector (VI) comprising (VI) (4) a host cell (VII) C comprising (VI) or (VI); (5) increasing (VI) the functional in vivo half-CC infe or the serum half-life of a parent protein C polypoptide. The conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and choosis, disseminated intravascular conjugation (III), sepsis, septic chock of the comprise of the conformation of the parent protein c polypoptide as not constituted intravascular constitution such as bone marrow shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARUS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a administration of less protein, and fewer side effects the risk of the currently available anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence represents a zymogen protein C variant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the protein C sequence appearing as AAU99002 and the information in claim 9 The invention relates to a conjugate (I) comprising at least one non-Sequence 419 AA;

Ş 뮹 S 밁 Local Similarity 121 417; Conservative 61 61  $\vdash$ APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120 SICCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSIDNGGCTHYCLEEVGWRRCSC 120 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60 ANSFLEELRHSSLERECIBEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 99.3%; Score 2308; DB 5; Pred. No. 3.3e-142; 0; Mismatches 2; 3.3e-142; ches 2; Indels 0 Gaps

60

Query Match

Length 419;

0

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241 181 181 121

KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240

300

KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW 300

SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD

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301 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360

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XX Human
XX Human;
XW Serum
XW Serum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular born; DIC; sepsis; septic shock; embolism; pulmonary embolism; born; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; both marrow transplantation; major surgery; trauma; ARDS; coagulant; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000; 2000DK-00001560.

18-OCT-2000; 2000US-0242268P.

21-UUN-2001; 2001DK-00000970.

21-UUN-2001; 2001US-0300154P.
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                                                                                                                                                                                                                                                                                                                                        Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-489875/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen KV, Pedersen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001WO-DK000679
                                                                                                                                                                                                                                                   Claim 9; Page; 92pp; English
                                                                                                                                                                                                                                                                                                                 attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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MAXYGEN HOLDINGS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type His substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild-type Leu substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Activation_peptide
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CC His/Lys/Arg/Asn/Asp/Giu/Giy/Gin; [2] a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) CC comprising (V) or (VI); (5) increasing (W2) the functional in vivo half-cC life or the serum half-life of a parent protein c polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, CC and in the manufacture of medicaments for the treatment (and coding of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased serum half-life, increased in increased in vivo half-life, increased trainsplantation for surgery/trauma or adult conjugate offers a number of advantages over the currently available conjugate offers a number of advantages over the currently available capt products, including longer duration between injections.

CC administration of less protein, and fewer side effects. Moreover, a dedication while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is not the conjugate has an extended plasma life. The gene for protein C sequence appearing as ANU99002 and the information in claim 9 cc constant of the invention. Note: The present sequence is not conjugate of a protein c sequence appearing as ANU99002 and the information in claim 9 cc conjugates of the conjugates in the specification but was created by the indexer using the conjugates of the conjugates and the information in claim 9 cc constant of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
361
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                                                                                                                                                                                                                                                                                                                                                                                                                  121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                          241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFLEELRHSSLERECIBEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                      GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVKLGEYDLRKWEKWELDLDI 240
                                                                                                        GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                      GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                          KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                            KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
  GGPMVAS FHGTWFLVGLVSWGEGCGNLTNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.3%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2307;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 419;
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                                                                                                                                                                                                                                                                                                                        240
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RESULT 130
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AAB82675 standard; protein; 419

AAB82675;

AAB82675
ID AAB
XX
AC AAB
XX
DT 15-15-0CT-2001

(first entry)

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Disulfide-bond
Disulfide-bond
Cleavage-site
                                                                                                                                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein C; human; coronary syndrome; unromwosar, ungarroagulation; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein C derivative (S11G/Q32E/N33D/L194S).
                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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 02-FEB-2000; 2000US-0179801P
                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                   19-JAN-2001; 2001WO-US000020
                                                                               Disulfide-bond
                                                                                          Disulfide-bond
                                                                                                                                  Modified-site
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                                                                                                                                                                                     Misc-difference
                                                           WO200157193-A2
                                                                                                             Modified-site
                                                                                                                                                                                                                                                                            120. .133
141. .277
156. .157
                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-glycosylated"
32
                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                              /note= "cleavage makes a 2-chain inactive precursor of amino acid light chain attached via a disulfide bond 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                               329
                                                                                                                                                                                                         169.
                                                                                                                                                                                                                                       158.
                                                                                                                                                                                                                 zymogen'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
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                                                                                                                                                                                                                                                                                                                                                      not e=
                                                                                                                                                                                                                                                                                                                                                                        note= "Gln in wild-type protein"
                                                                                                    note= "N-glycosylated"
                                                                                                                                           'note= "N-glycosylated'
                                                                                                                                                                          'note= "Leu in wild-type protein"
                                                                                                                                                                                               'note= "thrombin cleavage site"
                                                                                                                                                                                                                            note= "activation peptide; removal activates the 2-chain
                                                                                                                        note= "N-glycosylated
                                                                                                                                                                                                                                                                                                             .109
                                                                                                                                                                                                                                       . 169
                                                                                                                                                                .212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gla domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                                      "Asn in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                      "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "gamma-carboxylated"
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Matches 415;
                                      Query Match
                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a claimed human protein C derivative in which Ser at amino acid position 11 of the mature wild-type protein C sequence (see AAB2673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. The protein is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful
                                                                                                                           protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stemosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                             for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an antiplatelet agent or by local delivery through an intracoronary catheter),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-496919/54.
N-PSDB; AAH26363.
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                                                                                    Sequence 419
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                    Local
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 52-53; 63pp; English.
Conservative
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                    99.2%;
2;
                    Score 2306; DB 4;
Pred. No. 4.5e-142;
  Mismatches
  2;
                                             Length 419;
      Indels
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RESULT 131 AAR13537

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09-JAN-2003
31-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant mutants of human protein {\mathbb C} - having aminoacid changes for increased sensitivity to activation by thrombin and thrombin-thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         administered as a pro drug useful in prevention and treatment of diseases involving intravascular coagulation. It can also be given to thrombrotypenic patients with invasive cancers with effective and intensive chemotherapy. See also AAR13538-40 and AAR13623. (Updated on 09-UNA-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replaced by Asn. The zymogen can be activated in vivo by thrombin alone (even in the presence of calcium) and is more susceptible to activation by thrombin thrombomodulin than native HPC zymogen. Zymogen N can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein C Zymogen N comprises a signal peptide and propeptide of a gamma-carboxylated secreted protein, the light chain of HPC, a basic dipeptide (i.e. Lys-Arg, but can also be Arg-Lys, Lys-Lys or Arg-Arg) and amino acid residues 200-461 of HPC but with Ile(213) deleted and Asp(214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 37-38; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-254444/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPC mutant; pro drug; intravascular coagulation; zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 460 AA;
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                                                                                                                                                                                                                                                                                                                                             Local
                                      181
222
                                                                            163
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                                                                                                                                                                                                                                                                   1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                           Similarity
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                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDBSKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                        APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                               SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                           ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                            APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRL-NGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grinnell BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-00484133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Lys-Arg dipeptide
                                                                                                                                                                                                                                                                                                                                         99.2%;
                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                   Score 2304.5; DB 2;
Pred. No. 6.2e-142;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                              Length 460;
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                                                                                                                                                                                                                                                                                                                        Gaps
                                        240
                                                                                                                    180
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283
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AAB82676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein C; human; coronary syndrome; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein C derivative (S11G/Q32E/N33D/L194S/T254S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB82676 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anticoagulant;
                                        Peptide
                                                                                                                      Cleavage-site
                                                                                                                                       Disulfide-bond
                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                        Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; thrombolytic; cardiant; antianginal;
                                                                                                                    120. .133
141. .277
156. .157
                                                                                                                                                                                                                                                                                    /note= "Gln in wild-type protein"
33
/note= "activation peptide; removal activates the 2-chain {\tt zymogen"}
                                                       /note= "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                            /note= "N-glycosylated"
32
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                                                                                                                                                                                .109
                                                                                                                                                                                                                                                                                                                                                                                                                              "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-2000;
14-MAR-2000;
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a claimed human protein C derivative in which Ser at position 11 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser, and Thrat position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticogulant activity and resistance to inactivation by serpins compared anticogulant activity and resistance to inactivation by serpins compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-2001;
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                                                                                                                                                                                                                                                     for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an antiplatelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 53-54; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH26364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerlitz BE,
                                                                                                                                                                                                                        Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infarction, unstable angina, sepsis, throm thrombotic occlusion, and thromboembolism.
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                                                                                                                                                                   Local Similarity
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 52
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                                                                                               ANSFLEELRHSSLERECIBEICDFBEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHFCA 60
SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                    SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                         ANSFLEELRHGSLERECIEEICDFBEAKEIFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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2000US-0189197P.
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196. .212
248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Leu in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Thr in wild-type protein"
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                                                                                                                                                                 99.1%;
98.8%;
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                                                                                                                                                                   Score 2302; DB 4;
Pred. No. 8.2e-142;
                                                                                                                                                 Mismatches
                                                                                                                                                                                   Length 419;
                                                                                                                                                 Indels
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1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

Indels

0

Gaps

0

Query Match Best Local Matches

Local Similarity

415;

Conservative

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                                                            Protein C; truncated; thrombotic disorder; vascular disorder; stroke; hypercoagulable state; myocardial infarction; unstable angina; sepsis; adult respiratory distress syndrome; sickle cell anemia; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY56803 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Truncated human protein C polypeptide
                                                                                                      e.g. stroke; myocardial infarction; unstable angina; sepsis; adult respiratory distress syndrome; sickle cell anemia etc. The truncated protein C retains the activity of full-length protein C but does not
                                                                                                                                                    truncated heavy chain. The protein can be produced by standard recombinant methodologies. The truncated protein C is used to treat a wide range of thrombotic or vascular disorders or hypercoagulable states,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-1999.
                                                                                                                                                                                               This represents a human protein C polypeptide having a light chain and
                                                                                                                                                                                                                               Claim 2; Page 22-23; 23pp; English
                                                                                                                                                                                                                                                          Novel polypeptide useful for treating thrombotic and vascular diseases and hypercoagulation, e.g. stroke.
                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ46750
                                                                                                                                                                                                                                                                                                                                                      Huang L,
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9963070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                            Sequence 415 AA;
                                                                                         undergo C-terminal cleavage, of the heavy chain, during activation
                                                                                                                                                                                                                                                                                                                                                                                  (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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                                                                                                                                                                                                                                                                                                                                                      Riggin RM;
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98.9%; Score 2298; DB 3;
100.0%; Pred. No. 1.5e-141;
tive 0; Mismatches 0;
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                                   Length 415;
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                                                                                                                                                                                                                                                                                                                                                                                                 Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEVFVHENYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVIGW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
/note= "N-glycosylated"
32
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                           /note= "Gla domain"
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                                                                                                                                                                                                "Ser in wild-type protein"
                                       "gamma-carboxylated"
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14-MAR-2000; 2000US-0189197P.
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                            Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
                                                                                                                    N-PSDB; AAH26365.
                                                                                                                                                                                                                                                                                                                  19-JAN-2001; 2001WO-US000020
Claim 5; Page 54-55; 63pp; English.
                                       infarction, unstable angina, sepsis, throm thrombotic occlusion, and thromboembolism.
                                                                                                                                        WPI; 2001-496919/54.
                                                                                                                                                                              Gerlitz BE,
                                                                                                                                                                                                                   (ELIL ) LILLY & CO ELI
                                                                                                                                                                              Jones BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196.
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33
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59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "cleavage makes a 2-chain inactive precursor (155-
amino acid light chain attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Leu in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "N-glycosylated
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The present sequence is that of a claimed human protein C derivative in C which His at position 10 of the mature wild-type protein C sequence (see C ABB2673) is substituted with Gln, Ser at position 11 with Gly, Gln at C position 32 with Glu, Asn at position 33 with Asp, and Leu at position CC lay with Ser. It is an example of protein C derivatives of the invention CC that have at least 2 amino acid substitutions, but which have increased CC with the wild-type protein, while retaining the biological activity of CC the wild-type protein. A method of producing the biological activity of CC the wild-type protein. A method of producing the biological activity of CC trombosis (e.g. myocardial infarction and unstable angina), vascular CC coclusive disorders and hypercoagulable states, sepsis (in combination CC with bactericidal permeability increasing protein or with tissue factor CC with bactericidal permeability increasing protein or with tissue factor CC pathway inhibitor), thrombotic disorders (in combination with an antiplatelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
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   WPI; 2001-514662/56
                                                               Gerlitz BE, Grinnell BW,
                                                                                                                                                                                      11-FEB-2000; 2000US-0181948P
14-MAR-2000; 2000US-0189199P
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                                                                                                                          (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                   02-FEB-2001; 2001WO-US001221
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Pred. No. 1.5e-141;
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#XEEEX##555555555555555555555555555555
                                                                                                                                                                                           The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DiC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemodytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
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Query Match Best Local : protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative Sequence 419 AA; 98.8%; Score 2296; DB 4; Length 419; Pred. No. 2e-141;

Similarity

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                     GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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31-OCT-1991
                                         AAR13538;
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Human Protein C

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein C Zymogen FN comprises a signal peptide and propeptide of a gamma carboxylated secreted protein, the light chain of HPC, a basic dipeptide (i.e. Lys-Arg, but can also be Arg-Lys, Lys-Lys or Arg-Arg) and amino acid residues 200-461 of HPC but with Ile(213) deleted, Asp(209) replaced by Phe and Asp(214) replaced by Asn. The zymogen can be activated in vivo by thrombin alone (even in the presence of calcium) and is more susceptible to activation by thrombin/thrombomodulin than native HPC zymogen. Zymogen FN can be administered as a pro drug useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention and treatment of diseases involving intravascular coagulation. It can also be given to thrombocytopenic partients with invasive cancers with effective and intensive chemotherapy. See ARR19537-40 and ARR19621. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 460 AA;
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                   GYHSSREKEAKRNRTFVLNFIKIFVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 2.46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S)
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  Disulfide-bond
Modified-site
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/note= "Leu i
196. .212
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                                                                               194
                                                                                                                           169.
                                                                                                                                                                                                                        156. .157

/note= "cleavage makes a 2-chain inactive precursor (
amino acid light chain attached via a disulfide bond
262-amino acid heavy chain)"
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                                                                                                                                           zymogen"
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                                                                                                    /note= "thrombin cleavage site"
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                                                                                                                                                                     /note= "activation peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Gln in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "gamma-carboxylated"
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                                                      in wild-type protein"
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                                                                                                                                                                               removal activates the 2-chain
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                              coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in
                                                                                                                                                                                                                                                                                                                                                              Sequence 419 AA;
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                                                                                                                                                                                                                                                                                                          Local
                     181 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                         121
                                                                                             121
                                                                                                                                                                                                                                                                                    413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Page 56-57; 63pp; English.
                                                                                                                                 61
                                                                                                                                                                       13
                                                                                                                                                                                                             44
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                         ANSFLEELRQGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
Conservative
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98.6*;
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Pred. No. 2.7e-141;
3; Mismatches 3; Indels
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XX Human;
KW Human;
KW sickle
KW haemol
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                        cc molecules encoding such derivatives. These derivatives have increased canticoagulation activity, resistance to serpin inactivation and increased cesnsitivity to thrombin activation compared to wild type protein C. and control of the biological activity of the wild type human protein C. Protein C. derivatives are useful in the manufacture of a medicament for the current of acute coronary syndromes e.g. myocardial infarction and cunstable angina; and disease states predisposing to thrombosis; vascular coclusive disorders and hypercoagulable states e.g. disseminated contusive disorders and hypercoagulable states e.g. disseminated contusive cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing corotein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thrombosism or stenosis in coronary, cerebral or peripheral arteries continued to the combineral arteries are the combineral arteries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myccardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE08627 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein C derivative #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 46-47; 59pp; English.
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14-MAR-2000; 2000US-0189199P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thromboembolism; prothrombotic disorder; gene therapy; thalassaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human protein C derivatives and nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion;
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   WPI; 2001-514662/56
                                                                     Gerlitz BE,
                                                                                                                                                                                                11-FEB-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                  02-FEB-2001; 2001WO-US001221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thromboembolism; prothrombotic disorder; gene therapy; thalassaemia
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                                                                                                                                 (ELIL ) LILLY & CO ELI
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2000US-0189199P
                                                                  Grinnell BW,
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Pred. No. 4.9e-141;
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Matches Query Match

Local

al Similarity
413; Conserv

Conservative

2;

98.5%;

Score 2288; DB 4; Pred. No. 6.7e-141; Mismatches

Length 419; Indels

0

Gaps

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anticoacy control activity, resistance to serpin inactivation and increased constitutive to thrombin activation compared to wild type protein C. and CC retains the biological activity of the wild type human protein C. Protein CC derivatives are useful in the manufacture of a medicament for the constable angina; and disease states predisposing to thrombosis; vascular cocclusive disorders and hypercoagulable states e.g. disseminated cocclusive disorders and hypercoagulable states e.g. disseminated cocclusive disorders and hypercoagulable states e.g. disseminated contravascular coagulation (DIC), burns, transplantations, thalassaemia, combinated and transplantations, thalassaemia, computed the compared protein, thrombotic disorders in combination with an anti-platelet agent; corin combolism or stenosis in coronary, cerebral or peripheral arteries corin collecules of the invention are useful for treating humans with entering humans with predisposed prothin characterian derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD15228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased
Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 50-51; 59pp; English.
                                              present sequence is human protein C derivative
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                                                                                                                                                                                                   KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                          SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEBICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA
GGPMVAS FHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                           APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVFPRLIKGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFLEELROGSLERECIEBICDFEEAKEIFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                               GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRÓDÁCEGDS
                                                                                                               GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSBNMLCAGIIGDRQDACEGDS
                                                                                                                                                                KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWBKWELDLDI
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RESULT 140
AAE08628
ID AAE086
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      Human protein C derivative
                       01-NOV-2001
                                                    AAE08628 standard; protein; 419
                       (first entry)
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Best Local Sim
Matches 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina, and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemornhogic fever and haemorhic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein C deficiency; acute arrerial thrombotic occlusion, thromboembolism or stemosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein {\tt C} derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 47-48; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecules encoding such derivatives. These derivatives have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human protein C derivatives and nucleic acid
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                           SPWQVVILDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
SPWQVVLLDSKKKSACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVFPRLIKGKMTRRGD
                                                                                                                   APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSPLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                                                          ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA
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                                                                                                                                                                                                                                                                                                                         Conservative
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98.3%;
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                                                                                                                                                                                                                                                                                                                                                               Score 2286;
                                                                                                                                                                                                                                                                                                                       Mismatches
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Matches Query Match Best Local :

410;

Conservative

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Mismatches

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69 0;

10 HSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCASICCGHGTC

IDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDD 120

Local Similarity

98.1%; Score 2281; DB 7; 100.0%; Pred. No. 1.9e-140;

Length 410; Indels

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RESULT 141
ADC40012
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                                                          protein C (aPC), a chelating agent and optionally a diluent. The composition of the invention is useful for treating thrombotic disorde such as: intravascular coagulation, thrombotic stroke, deep vein thrombosis, pulmonary embolism, peripheral arterial thrombosis, acute myocardial infarction and retina thrombosis. The present amino acid
                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2002; 2002US-0363364P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intravascular coagulation; thrombotic stroke; deep
pulmonary embolism; peripheral arterial thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human activated protein C-related protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC40012 standard;
Sequence 410 AA;
                                                                                                                                       The invention comprises a pharmaceutical composition containing activated
                                                                                                                                                                            Disclosure; SEQ ID NO 1; 29pp; English
                                                                                                                                                                                                       Pharmaceutical composition comprising activated protein C and a chelating agent useful for treating thrombotic disorders such as stroke, deep vein thrombosis, pulmonary embolism and myocardial infarction.
                                                                                                                                                                                                                                                                        WPI; 2003-722308/68
                                                                                                                                                                                                                                                                                                        Gopalrathnam G,
                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2003; 2003WO-US005046
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003075834-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute myocardial infarction; retina thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; activated protein C; aPC; thrombotic disorder;
                                             sequence represents a human protein that was used in the exemplification
                               of the invention.
                                                                                                                                                                                                                                                                                                                                        (ELIL ) LILLY & CO ELI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS
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                                                                                                                                                                                                                                                                                                      Huang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 410
                                                                                                                                                                                                                                                                                                        Riggin RM,
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                                                                                                                                                                                                                                                                                                         Sheliga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deep vein thrombosis;
                                                                                                                   disorders
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RESULT 142
ADC40013
ID ADC4001
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Matches 408;
                                 Best Local Similarity
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human activated protein C-related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC40013 standard; protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intravascular coagulation; thrombotic stroke; deep vein thrombosis; pulmonary embolism; peripheral arterial thrombosis;
                                                                                                                           Sequence
                                                                                                                                                                                                                                                      myocardial infarction
                                                                                                                                                                                                                                                                                                                                             The invention comprises a pharmaceutical composition containing activated protein C (aPC), a chelating agent and optionally a diluent. The composition of the invention is useful for treating thrombotic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 2; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pharmaceutical composition comprising activated protein C and a chelating agent useful for treating thrombotic disorders such as stroke, deep vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-722308/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2002; 2002US-0363364P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003; 2003WO-US005046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; activated protein C; aPC; thrombotic disorder;
                                                                                                                                                                                                                  such as: intravascular coagulation, thrombotic stroke, deep vein thrombosis, pulmonary embolism, peripheral arterial thrombosis, acute myocardial infarction and retina thrombosis. The present amino acid sequence represents a human protein that was used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gopalrathnam G, Huang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute myocardial infarction; retina thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                                                                                          invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWBKWELDLDIKEVFVHPNY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLD 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKRINRTEVLINFIKI PVVPHINECSEVMSIMVSENMLCAGILGDRODACEGDSGGPMVASFH
                                                                                                                           409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pulmonary embolism and myocardial infarction.
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                              97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riggin RM,
1; Mismatches
                              Score 2270; DB 7;
Pred. No. 9.6e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheliga TA;
                                                            Length 409;
      Indels
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Conservative

Gaps

Protein C Zymogen SC comprises a signal peptide and propeptide of a gamma carboxylated secreted protein, the light chain of HPC, a basic dipeptide (i.e. Lys-Arg, but can also be Arg-Lys, Lys-Lys or Arg-Arg) and amino

Disclosure; Page 12 and Table 1; 67pp; English

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RESULT 143
AAR13623
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31-OCT-1991
                                                                   Recombinant mutants of human protein {\tt C} - having aminoacid changes increased sensitivity to activation by thrombin and thrombin-thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            Human Protein C zymogen SC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13623 standard;
                                                                                                                                             Gerlitz BE,
                                                                                                                                                                                                                      22-FEB-1991;
                                                                                                                                                                                                                                              28-AUG-1991.
                                                                                                                                                                                                                                                                    EP443875-A.
                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                   HPC mutant;
                                                                                                                                                                     (ELIL ) LILLY & CO ELI
                                                                                                                                                                                             23-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 DGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SSLERECIEEICDFEEAKQIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCCGHGTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWPLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRINTIFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGBYDLRRWEKWELDLDIKEVFVHPNYS
                                                                                                                                                                                                                                                                                                                                                                   pro
                                                                                                                                               Grinnell BW;
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                              90US-00484133
                                                                                                                                                                                                                      91EP-00301450
                                                                                                                                                                                                                                                                                                                                                                   drug; intravascular coagulation; zymogen.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                            /label= Lys-Arg dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 460 AA
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RESULT 144
AAP93714
ID AAP937
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 460 AA;
   12-JUN-1987;
                                                                09-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; anticoagulant; protein-C; Factor-X; Gla domain; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid protein of protein-C and Factor-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP93714 standard; protein; 461
                                                                                                                                 28-DEC-1988
                                                                                                                                                                                              EP296413-A.
                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPWQVVILIDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPMVÄSFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHSSREXEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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(first entry)
   87JP-00145293
                                                                88EP-00109186
                                                                                                                                                                                                                                                 1. .40
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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97.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a fusion protein in which the Gla domain of protein is replaced with that of Factor X. The novel protein has a more potent anticoagulation activity than protein. C and is expected to have competitive inhibitory activity against menadione dependent blood coagulation proteins. It also has neutralization activity against plasminogen activation inhibitor, and inactivates Factor-Va or Factor-VIIIA. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybrid protein of protein C with replaced Gla domain - using human vitamin=K dependent proteins, e.g. factor X, to give improved anticoagulation activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 16-19; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 96.6%;
Local Similarity 95.7%;
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                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                   GYHSSREKEAKRURTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                               KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVFICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                    SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 160
                                                                                                                                                                                                                                                                                                                                                               SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                         ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKHVDGDQCLVLPLEHPCA 100
                                                                 GYHSSREKEAKRNRTFVLNFIKI ÞVVÞHNECSEVMSNMVSENMLCAGILGDRÓDACEGDS
                                                                                                                                   KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQBILVIGW 340
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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Pred. No. 5.3e-138;
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RESULT 145
AAW72753
ID AAW72753;
XX
AC AAW72753;
AC AAW72753;
XX
DT 08-JAN-1999 (first entry)
XX
DT 08-JAN-1999 (first entry)
XX
Expression of activated human protein C.
XX
DE Primary structure of activated human protein C.
XX
DE Primary structure of activated human protein C.
XX
DE Primary structure of activated human protein C.
XX
DE Primary structure; autodegradation;
XX
DE Primary activated protein C; primary structure; autodegradation;
XX
DE Primary human; activated protein C; primary structure; autodegradation;
XX
DE Primary structure; autodegradation;
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DE Primary human; activated protein C; primary structure; autodegradation;
XX
DE Primary human; activated protein C; primary structure; autodegradation;
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DE Primary human; activated protein C; primary structure; autodegradation;
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DE Primary human; activated protein C; primary structure; autodegradation;
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DE Primary human; activated protein C; primary structure; autodegradation;
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DE Primary human; activated protein C; primary structure; autodegradation;
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Disulfide-bond
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Miso-difference 162
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Misc-difference 159
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
Misc-difference 158
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Disulfide-bond
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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Disulfide-bond
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An improved method has been developed of of activated protein \mathbb C (aPC). The method
                                                                                                                                                                      04-NOV-1998.
                                                                                                                                                                                        EP875563-A2
                                                                                                                                                                                                         Disulfide-bond
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                                                                                                                                  28-APR-1997;
                                                                                                                                                    28-APR-1998;
                          Disclosure; Fig 1; 7pp; English
                                          Improved processing and purification of activated protein C - processing aqueous solution at specified ionic strength and pithe amount of autodegradation products.
                                                                                                Carlson AD,
                                                                              WPI; 1998-559430/48.
                                                                                                                 (ELIL ) LILLY & CO ELI
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                                                                                              Sheliga TA,
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17. .22
50. .69
80. .89
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105. .118
120. .133
                                                                                                                                   97US-0045255P
                                                                                                                                                    98EP-00303312
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331. .345
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168
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                processing at an ionic strength greater than 150 mM and a pH of 5.5-6.3. The present sequence represents the primary structure of activated human protein C, used to assist in illustrating the autodegradation pathways described in the present invention. The apc is used for treating a variety of acquired disease states involving intravascular coagulation e.g. thrombotic stroke, deep vein thrombosis, pulmonary embolism, peripheral arteries, acute myocardial infarction, disseminated intravascular coagulation and acute pre- or postcapillary occlusions including transplantations or retina thrombosis. The process minimises the process minimises the process minimises.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the percentage of autodegradation products forming at most 10%, preferably below 5% of des(1-9) aPC and des(1-10) aPC by weight, to achieve a more potent, higher purity aPC pharmaceutical preparation
361
                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                    SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA
                                                                                                                                                                      KEVFVHENYSKSTIDNDIALLHLAQPATISQTIVEICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                        SPWQVVLLDSKKKLACGAVLIHESWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                     SLCCGHGTCIDGIGS FSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKBAPQKSWAP
                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                   GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                                                     SPWQVVLLDSXKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWBKWELDLDI
                                                                                                                                                                                                                                                                                               ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA
                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS
                                                                                                                                               KEVFVH PNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLABRELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2210; DI
Pred. No. 7.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
.8e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 419;
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RESULT 146
AAR13083
25-MAR-2003
30-SEP-1991
                                                                                                                                                        AAR13083;
                                                                                                                                                                        AAR13083
                                                                                      gla-domain; VKDP.
                       Protein
                                                                       Homo sapiens
                                                                                              Phopholipid; binding protein; lipocortin; domain; vitamin
                                                                                                               PAP-I-protein C fusion construct.
                                               Protein
                                                                                                                                                                        standard;
                                                                                                                                (revised)
(first entry)
                         /note= "amino acids 1-136"
137. .509
                                                       Location/Qualifiers
         /label= protein_C
/note= "amino acids 46-136'
                                        /label= PAP-I
                                                                                                                                                                        protein; 509
                                                                                                                                                                        ΑA
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K; PBP;

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AAY49558
ID AAY4
XX
AC AAY4
XX
DT 13-0
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XX
                                                                                                                                                                       RESULT 147
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Best Local S:
Matches 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The fusion was constructed using site-directed mutagenesis to fuse PAP-I encoding amino acid 1-136 with a protein C DNA sequence at the codon for amino acid 46. A plasmid contg. this construct was transfected into BHK cells which were then cultured to produce PAP-I-protein C fusions which were activated to a form fully active in both amidolytic and anticoggulant assays. See also AAQ12678-81. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09109953-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant prodn. of hybrid phospholipid-binding proteins - comprising lipocortin phospholipid-binding domain and vitamin=K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ12680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1989;
                 Human protein C protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct PA field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC
                                                         13-JAN-2000
                                                                                                                                 AAY49558 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ASLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 ELKHALKGAGTNEKVLTETIASRTPEELRAIKOVYEEE---YGSSLDGDQCLVLFLEHPC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEXDLRRWEKWELDLD
                                                                                                                                                                                                                                                     SGGPMVASFHGTWFLVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWA 418
                                                                                                                                                                                                                                                                                                       WGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGD
                                                                                                                                                                                                                                                                                                                               WGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGD
                                                                                                                                                                                                                                                                                                                                                                                 IKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTG
                                                                                                                                                                                                                                                                                                                                                                                                                     IKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSPWQVVLLDSKKKLACGAVLTHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPGYKLGDDLLQCHPAVKFPCGRPWKRMBKKRSHLKRDTEDQEDQVDPRLIDGKMTRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELRHS----SLERECIEEICDF--EEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPC
                                                                                                                                                                                                                             SGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%;
91.4%;
                                                                                                                               protein;
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Pred. No. 1.3e
9; Mismatches
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1.3e-127;
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 RESULT 148
AAR12196
ID AAR121
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ32159 to AAZ32194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic analysis.

AAY49550 to AAY49573 represent the proteins which correspond to some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; coding sequence polymorphism; vascular pathology gene; polymorphic site; phenotype correlation; forensic; paternity testing; medicine; genetic analysis; vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predisposition to vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determination of polymorphisms in genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the reference alleles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                   AAR12196 standard; protein; 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                     VASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                   VHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHS
                                                                                                                                                                                                                                                                                                                                                                                 VVLIDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVF
                                                                                                                                                                                                                                                                                                                                                                                                                       KLGDDLIQCHPÄVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDFRLIDGKMTRRGDSPWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGDSPWQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSCAPGY 124
                                                                                                                                                                                           SREKEAKRIRTFYLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPM
                                                                                                                                                                                                                 SREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDSGGPM 364
                                                                                                                                                                                                                                                                   VHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHS
                                                                                                                                                                                                                                                                                                                                               VVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVF 181
                                                                                                                 VASTHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.9%; Score 1972; DB 2; ilarity 100.0%; Pred. No. 2e-120; Conservative 0; Mismatches o
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09-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein C catalytic domain mutant E(213)->R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR12196;
                                                                                                                                                                                                                                      The mutant has a prolonged half-life in blood compared with natural activated human protein C. Alternative positions for substns. are Asp(20), Lys(22), Lys(23), Lys(24), Asp(45), Lys(48), Lys(490), Asp(182), Asp(183), Asp(185) and Trp(211). The amino acid is replaced with an oppositely charged residue. The active site amino acids, His(42), Asp(88), and Ser(191) must be present. See also AAR11838 and AAR12192-R12195. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP03072877-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Active-site
                                                                                                                                                                                                                       Sequence 262 AA;
                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                  Activated human protein C deriv. and DNA encoding it - has prolonged blood half life for use as an anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-1989;
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241
                                                                                                                                                          158 DTEDQEDQVDPRLIDCKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK 217
                398
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                                                   338
                                                                      121
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                                                                                                                                                                                   260;
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                                                                                                                                                                                            Similarity
RYLDWIHGHIRDKEAPQKSWAP
                                                                                      LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN
                                                                                                          KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC
                                                                                                                        KLLVRLGEYDLRRWEKWELDLDIKEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPIC
                                                                                                                                               DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK
                                   MVSENMLCAGI
                                                   MVSENMLCAGILGDRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVS
                                                                      LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNNTFVLNFIKIPVVPHNECSEVMSN
              RYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                   Conservative
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(first entry)
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191
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1. .12
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27. .54
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                                   LGDRODACEGDSGGPMVASFHGTWFLVGLVSWGRGCGLLHNYGVYTKVS
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                                                                                                                                                                                  Score 1409; DB 2;
Pred. No. 5.8e-84;
0; Mismatches 2
262
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                                                                                                                                                                                                     DB 2;
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AAR12193
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338 MVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVS 397
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Matches 260;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   The mutant has a prolonged half-life in blood compared with natural activated human protein C. Alternative positions for substns. are Asp(20), Lys(22), Lys(23), Lys(24), Asp(45), Lys(49), Lys(49), and Asp(185), Trp(211) and Glu(213). The amino acid is replaced with an oppositely charged residue. The active site amino acids, His(42), Asp(88), and Ser(191) must be present. See also ARR11838 and ARR12192-R12196. (Updated on 25-MAR-2003 to correct PA field.)
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09-JUL-1991
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Disulfide-bond
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                    278 LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIFVVPHNECSEVWSN
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                                                                                                              XLLVRLGEYDLRRWEKWELDLDIXEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC
                                                                                  KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC
LPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNNTFVLNFIKIPVVPHNECSEVMSN
                                                                                                                                                                         DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK
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99.2%;
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Pred. No. 7.9e-84;
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RESULT 150
AARI1838

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Best Local Similarity
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Disulfide-bond
Active-site
Disulfide-bond
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09-JUL-1991
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                                                                                                                                                                                                             The mutant has a prolonged half-life in blood compared with natural activated human protein C. Alternative positions for substrms. are Asp(20), Lys(22), Lys(23), Lys(34), Lys(49), Asp(182) and Arg(183), Asp(185), Trp(211) and Glu(213). The amino acid is replaced with an oppositely charged residue. The active site amino acids, His(42), Asp(88), and Ser(191) must be present. See also AAR12192-R12196. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                Activated human protein C deriv. and DNA encoding it - has prolonged blood half life for use as an anticoagulant.
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                                                                                                                                                                                  Sequence 262 AA;
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              218 KLIVELGEYDIARWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC 277
                                                                        158 DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK 217
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                                                           DTEDQEDQVDPRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMRESK 60
KLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPIC 120
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191
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99.2%;
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                                                                                                                                     Score 1406; DB 2;
Pred. No. 9.1e-84;
                                                                                                                     Mismatches
                                                                                                                                                   Length 262;
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      QY
      278 LPDSGLAERELNQAGQETLYTGWGYHSSREKEAKRURTFYLNEIKTPVVPHNECSEYMSU 337

      Db
      121 LPDSGLAERELNQAGQETLYTGWGYHSSREKEAKRUNTFYLNEIKTPVVPHNECSEYMSU 180

      QY
      338 MYSENNLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGYYTKVS 397

      Db
      181 MYSENNLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGYYTKVS 240

      QY
      398 RYLDWIHGHIRDKEAPQKSWAP 419

      QY
      398 RYLDWIHGHIRDKEAPQKSWAP 262
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Search completed: June 14, 2004, 17:48:23 Job time : 69 secs

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CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
Search completed: June 2, 2004, 16:58:16 Job time: 28 secs
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Best Local Similarity
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                                                               361 GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419
361 GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPOKSWAP 419
                                                                                                                              301 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                             GYHSSREKBAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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nilarity 98.6%;
Conservative
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Local Similarity

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RESULT 13
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NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
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                              GYHSSREKEAKRURTFYLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS
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Pred. No. 5.3e-188;
3; Mismatches 3;
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3; Mismatches 3;
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PRIOR FILLING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILLING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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TYPE: PRT
ORGANISM: Homo s
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Local Similarity 98.6%;
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                          GGPMVASFHGTWFLVGLVSWGBGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                              GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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Pred. No. 7e-188;
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; Sequence 6, Application US/10182263
; Patent No. 6630138
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611

RESULT 15 US-10-182-263-6

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APPLICANT: Garner;
APPLICANT: Temperic
APPLICANT: Temperic
APPLICANT: Foster;
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Best Local (
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:
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TELEPAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: PRUNKARD, DONNA E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
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REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                            SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 162
 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWA 460
                                                                          GYHSSREKEAKRIRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRODACEGDS 402
                                                                                                                                                  KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQBTLVTGW 342
                                                                                                                                                                                                                                                                                                  APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 222
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; Pred. No. 3.9e-190;
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RESULT 11
US-10-182-263-5
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5270178-17
                                                                                               APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.;
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
ZYMOGEN FORMS OF HUMAN PROTEIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Geriltz, Bruce E
APPLICANT: JONES, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                            ;Patent No.
SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 5
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CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
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                                      NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                       FILING DATE: 23-FEB-1990
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98.8%;
                                            US/07/484,133
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Pred. No. 2.2e-188;
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LENGTH: 461

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PATENT NO. 5460953

PATENT NO. 5460953

APPLICANT: GERLITZ, BRUCE B.;GRINNELL,
TITLE OF INVENTION: VECTORS AND COMPOUN
GLYCOSYLATION MUTANTS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION NUMBER: US/08/93,217
FILING DATE: 09-SEP-1993
FRIOR APPLICATION NUMBER: 628,063
PRIOR APPLICATION NUMBER: 628,063
FRILING DATE: 21-DEC-1990
APPLICATION NUMBER: 484,081
FILING DATE: 23-FEB-1990
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5460953-3
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                                        Sequence 2, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
APPLICANT: Garner, Ian
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Best Local
              APPLICANT:
 APPLICANT:
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Local Similarity 99.8%;
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Cottingham, Ian R. Temperley, Simon M Foster, Donald C.
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Pred. No. 3.2e-190;
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NDS FOR EXPRESSION
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US-08-756-506-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 95-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                  361
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                              GGPMVAS FHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWA
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                                                                      GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSBVMSNMVSENMLCAGILGDRQDACEGDS
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Prunkard, Donna B.
VENTION: PROTEIN C PRODUCTION IN TRANSGENIC
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RESULT 10 US-08-756-506-4 ; Sequence 4, Application US/08756506 ; Patent No. 5905185

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       CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/18919
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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US-10-182-263-2
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Best Local (
SEQ ID NO 2
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                                                                                                                                                                                                                        Sequence 2, Application US/10182263 Patent No. 6630138
                                                                                                                             APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
FILE REFERENCE: X-13611
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LOCATION: 158..169
OTHER INFORMATION: OTHER INFORMATION: I
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LOCATION:
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LOCATION: 170..419
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100.0%; Pred. No. 8.7e-191;
tive 0; Mismatches 0;
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Peptide"
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TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID; PHOSPHOLIPID-BINDING PROTEINS
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CURRENT APPLICATION DATA:
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FILING DATE: 29-DEC-1989
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                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                            APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                           SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEBVGWRRCSC 162
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KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                         SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2324; DB 6; 100.0%; Pred. No. 9.8e-191;
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CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIVATE: Patentin version 3.1
SEQ ID NO: 1
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US-10-182-263-1
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-182-263-1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10182263
Patent No. 6630138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 00/045,255
PRIOR FILING DATE: 1997-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
                                                                                                                                                                                                                                                                    APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
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ORGANISM: Homo sapiens
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                                                           LENGTH: 419
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Local Similarity 100.0%; F
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Pred. No. 8.7e-191;
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PCT-US92-10242-1
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GENERAL INFORMATION:
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Best Local Similarity
TELEPHONE: 619-554-293
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18.NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serin
TITLE OF INVENTION: Anti-
TITLE OF INVENTION: for I
                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                  REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                     NAME: Fitting, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                     619-554-2937
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                            US 07/793,989
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Pred. No. 8.
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SEQUENCE CHARACTERISTICS:

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US-08-955-471-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
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NAME/KEY:
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Then
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 170..419
OTHER INFORMATION:
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APPLICATION NUMBER: US/08/955,471 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                   ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5968751th Torrey Pines Road, TPC
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Pred. No. 8.7
0; Mismatches
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Best Local (
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APPLICATION NUMBER:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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HYPOTHETICAL:
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LOCATION: 158..169
OTHER INFORMATION: OTHER INFORMATION: I
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LOCATION: 170..419
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                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
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                                                                                      GYHSSREKEAKRURTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS 360
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                GYHSSREKEAKRNRTFVLNFIKÍ ÞVVÞHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                  KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                               KEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
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Pred. No. 8.7e-191;
; Mismatches 0;
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; Sequence 3, Application US/0967570A; Patent No. 6436397
; GRUERAL INFORMATION:
; APPLICANT: Baker, Jeffrey C

US-09-667-570A-3

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Patent No. 5270178 Sequence 51, Appl Patent No. 5270178 Patent No. 5270178

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Minimum DB
Maximum DB
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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1: /cgn2 6/pcodata/2.

2: /cgn2 6/pcodata/2.

3: /cgn2 6/pcodata/2.

4: /cgn2 6/pcodata/2.

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INDERMATION POR EED IN NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 419 amino acids TYPE: amino acid TOPOLOSY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: NAME/KEY: Region LOCATION: 1.157	CITY: La Jolla STATE: CA STATE: CA COUNTRY: USA ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC compatible COMPUTER: LBM PC compatible COMPATING SYSTEM: PC-DCS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/295,411 FILING DATE: 22-AUG-1994	US-08-295-411-1  Sequence 1, Application US/08295411  Patent No. 5679639  GENERAL INFORMATION:  APPLICANT: Griffin, John H.  APPLICANT: Mesters, Rolf M.  TITLE OF INVENTION: Serine Protease-Derived Polype  TITLE OF INVENTION: Anti-Peptide Antibodies, Syste  TITLE OF INVENTION: for Inhibiting Coagulation  NUMBER OF SEQUENCES: 10  CORRESPONDENCE ADDRESS:  ADDRESSEE: Office of Patent Comsel, The Scripps  ADDRESSEE: Research Institute  STREET: 10666 No. 5679639th Torrey Pines Road, T
	1.25	Polypeptides and Systems and Therapeuti on scripps

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Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Patent NO. 5270178 Sequence 2, Appli Sequence 2, Appli Patent NO. 5270178 Patent NO. 5270178

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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                             NCBI_TaxID=10090;
                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                           Coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                054740
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PR00722; CHYMOTRYPSIN.
PR000010; EGFBLOOD.
PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         سو
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3; BS00010; ASX HYDROXYL; 1.
3; BS00022; EGF_1; 1.
5; PS01186; EGF_2; 2.
6; PS01187; EGF_CA; 1.
6; PS0011; GLU CARBOXYLATION; 1.
6; PS50240; TRYPSIN HIS; 1.
6; PS00134; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00179; EGF_CA; 1.
SM00069; GLA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMNVAPACLPQKDWAESTL--MTQKTGIVSGFG--RTHEKGRQSN---ILKMLEVPYVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYGIYTKVTTFLKWIDRSMKARVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTCKLSTSFSITQNMFCAGYEAKLEDACQGDSGGPHVTRFKNTYYVTGIVSWGEGCARKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHCMDESKKILLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELLNLNETQPERSSDDLVRIVGGRECKDGECFWQALLINEDNEGFCGGTILNEFYILTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGYFLGNDGKSCISTAPFPCGKITTGRRKRSVALNTSDSELDLEDALLDEDPLSPTENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKK-----RSHLKRDTED---QEDQVDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --CONOGACRDGIGGYTCTCSEGFEGKNCELFVRKL-CRLDNGDCDQFCREEQNSVVCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 AA;
                                                                                                                                                                                                                                           (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
factor X precursor (EC 3.4.21.6).
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%;
36.4%;
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Pred. No. 1.3e-67
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COAGULATION FACTOR X.

BAC09DE5EF9D271E CRC64;
                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                         Murinae; Mus.
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RR GG; GG:00046821; C:extrachromosomal DNA; IEA.
RR GG; GG:0003804; F:blood coagulation factor X activity; IEA.
RR GG; GG:0005509; F:calclum ion binding; IEA.
RR GG; GG:0005239; F:calclum ion binding; IEA.
RR GG; GG:000623; F:chymotrypsin activity; IEA.
RR GG; GG:000623; F:peptidase activity; IEA.
RR GG; GG:0004295; F:trypsin activity; IEA.
RR GG; GG:0004295; F:trypsin activity; IEA.
RR GG; GG:0004295; F:trypsin activity; IEA.
RR GG; GG:0004295; F:trypsin activity; IEA.
RR GG; GG:0004295; F:trypsin activity; IEA.
RR InterPro; IPR00151; Asx Eydroxyl S.
RR InterPro; IPR00152; Asx Eydroxyl S.
RR InterPro; IPR001801; EGF GI.
RR InterPro; IPR001801; EGF II.
RR InterPro; IPR001801; EGF II.
RR InterPro; IPR001326; BGF GIA blood.
RR InterPro; IPR002339; GIA blood.
RR InterPro; IPR002339; GIA blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00179; EGF CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; TATP SPC; 1.
SMART; SM00020; TATP SPC; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS00131; GLU CARBOXYLATION; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98454993; PubMed=9783672; Heidtmann H.H., Kontermann R.E.;
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_G1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00001; GLABLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA
AHCMDESKKLLVRLGEYDLRRWEKWELDLDI KEVFVHPNYSKSTTDNDI ALLHLAQPATL
                                                                                                                                                                                                                                                                                                                       SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKYKDGDQCESSP----
                                                IELLNLNETQPERSSDDLVRIVGGRECKDGECPWQALLINEDNEGFCGGTILNEFYILTA
                                                                                                                                                             ASGYFLGNDGKSCISTAPFPCGKITTGRRKRSVALNTSDSELDLEDALLDEDFLSPTENP
                                                                                                                                                                                                              APGYKLGDDLLQCHPAVKFPCGRPWKRMEKK-----
                                                                                                                                                                                                                                                                    --CONQGACRDGIGGYTCTCSEGFEGKNCELFVRKL-CRLDNGDCDQFCREEQNSVVCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA10933.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
481
53986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.1%; Score 793; DB 11; 36.4%; Pred. No. 1.6e-67; tive 77; Mismatches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WW;
                                                                                                       RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAGULATION FACTOR CF702DE5EF9D97AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158;
                                                                                                                                                                                                                   -RSHLKRDTED---QEDQVDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                         271
                                                                                                               209
                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                   120
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Q804X7
В
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                                                                                                                                                                               Matches
                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                          SMART; SM00181; EGF; 2.

SMART; SM00179; EGF CA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00021; ASX HYDROXYL; 1.

PROSITE; PS01002; EGF C; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS00114; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:0003802; F:blood coagulation factor VII activity;
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coagulation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q804X7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q804X7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004295; P:trypsin activity; IEA
GO; GO:0006508; P:proteolysis and peptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulation genes from Gallus gallus and Fugu rubripes."
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davidson C.J., Hirt R.P., Lal
Tuddenham E.G.D., McVey J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
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                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                              Hydrol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m; PF00594; gla; 1.
m; PF00599; trypsin; 1.
NTS; PR00722; CHYMOTRYPSIN.
NTS; PR00010; EGFBLOOD.
NTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF465268; AAO33363.1;
                                                                                                                                                                                 162;
93
                                        13
                                                                                     41
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                                                                                                                                  ш
                                                                                                                                                                                                       Similarity
                                                                                                                             ANSPLEELRHSSLERECIEBICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001881;
IPR001438;
SPCQNGGSCDDQFQDYVCRCPPEYEGKSCETAVAENLKCIYDNGGCEQYCADEQSEKRVC
                                        SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVS-FINCSIDNGGCTHYCLEEVGWRR-C 118
                                                                                     ANSFFEEIXLGPLERECIEEKCSFEEAREIYRDDERTKEFWHIYSDPNQC------DS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR009003;
                                                                                                                                                                                                                                                                         425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 25, Last annotation update) factor VII precursor (EC 3.4.21.21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteolysis and peptidolysis;
2; Asx_hydroxyl_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Peptidase S1.
; Peptidase S1A.
; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF Ca.
EGF Iike.
EGF like.
GLA blood.
                                                                                                                                                                                                                                                                           47626 MW;
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EGF_2.
                                                                                                                                                                                                    34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24,
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                                                                                                                                                                                 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                       Score 799.5;
Pred. No. 3.2
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                                                                                                                                                                                                                                                                         36A69BF0DB8C6DAC CRC64;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425
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                                                                                                                                                                                                         .2e-68;
                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                    146;
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                                                                                                                                                                                      Indels
                                                                                                                                                                                                                              Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEA.
                                                                                                                                                                                 31;
                                                                                                                                                                                      Gaps
                                                                                                                                         60
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RESULT
088947
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STRAIN=C57BL6 X CBA; TISSUE=Liver;
MEDLINE=98347933; PubMed=9684791;
Liang Z. Cooper A., DeFord M.E.,
Castellino F.J., Rosen E.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coagulation F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    088947;
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                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008295; F:trypsin activity; IEA.
GO; GO:0004295; F:proteolysis and peptidolysi
GO; GO:0006508; P:proteolysis and peptidolysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003
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                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                 MGD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF211347; AAP22980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP087644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thromb. Haemost. 0:0-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of a factor X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01
                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooper A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thromb. Haemost. 80:87-91(1998).
                                                                                                                                                      InterPro;
                                                                                                                                                                                                 InterPro;
                                                                                                         InterPro;
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; Peptidase_S1A.
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Kinoshita S., Iida H.,
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Mammalia; Eutheria;
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SMART; SM00020; Tryp SPc; 1.
PR0SITE; PS00135; TRYPSIN_SER; 1.
PR0SITE; PS00135; TRYPSIN_SER; 1.
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                                        EMBL; X79807; CAA56202.1; -. PIR; S49075; EXRT.
                                                                                                        carboxylase.";
Thromb. Res. 80:63-73(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro, IPR001254; Peptidase_S1.
InterPro, IPR0013114; Peptidase_S1A.
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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GO:0004263; F:chymotrypsin activity; IEA.
GO:0004295; F:trypsin activity; IEA.
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           P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLA
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23315 MW; 9D114E6D7FF5A9AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.1%;
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Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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R InterPro; IPR006209; EGF Ii.

InterPro; IPR00233; GLA blood.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR000394; Vitx Angelians, PF00008; Pon
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Best Local
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SMART; SM0019; GIA; 1.

SMART; SM00020; Tryp SPc; 1.

SMOSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS001186; EGF C; 2.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS001181; EGF CA; 1.

PROSITE; PS00101; GLU_CARBOXYLATION; 1.

PROSITE; PS00101; TRYPSIN LOM; 1.

PROSITE; PS001013; TRYPSIN HIS; 1.

PROSITE; PS001015; TRYPSIN SER; 1.

PROSITE; PS001015; TRYPSIN SER; 1.

PROSITE; PS001015; TRYPSIN SER; 1.
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InterPro;
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Pfam; PF00089; trypsin; 1.
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InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
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445 GKYGIYTKVTAFLKWIDRSMKARVGP 470
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PR00010; EGFBLOOD.
PR00001; GLABLOOD.
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                                                                                                                                                      HNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASPHGTWFLVGLVSWGEGCGLL
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                                                     HNYGVYTKVSRYLDWIHGHIRDKEAP 413
                                                                                                         RNTCRLSTSPSITQNMFCAGYDAKQEDACQGDSGGPHVTRPKDTYFVTGIVSWGEGCARK
                                                                                                                                                                                                                     FRENVAPACLPOKUWABATL--MTOKTGIVSGFGRTHEKGROSK-
                                                                                                                                                                                                                                                                  LSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVP
                                                                                                                                                                                                                                                                                                                        AAHCLHQAKRFKVRVGDLNTEQEDGGEMVHEVDMIIKHNKFQRDTYDFDIAMLRLKTPIT
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Peptidase_S1A.
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0284678E3954A698 CRC64;
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01-MAR-2003 (TrEMBLrel.
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                                                                    aracnydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio)
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SMART; SM00020; TTYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DON; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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                                                   NCBI_TaxID=7955;
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Pred. No. 1.
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RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Moriguez A.C., Grimwood J., Schmutz J., Nyers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                   264 PVKOHISHPQYNPITVDNDIALLRLDGPVKFSTYILPACLPSLELAKRMLHRNGTVTIIT
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                                   DSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSW 417
                                                                                                                                                                                                      DIKEVFVHENYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVT 298
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                                                                                  GWG----KNNQSATSYNSTLHYVELPIVDNKECSRHWMNNLSDNMLCAGVLGQVKDACEG
                                                                                                                          GWGYHSSREKEAKRNRTFVLNFIKIFVVPHNECSEVMSNMVSENMLCAGILGDRQDACEG 358
DSGGPMMTLFHDTWFLVGLVSWGEGCGQRDKLGIYTKVASYLDWI
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Pred. No. 3.7e-85;
70; Mismatches 131;
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RESULT 7
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM;
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M., Wada Nono M., Dongchon K., Hamasaki N.;
"Gene Analysis of Anticoagulation Factors in Japanese Thrombotic Patients. Genetic Background of Thrombophilia in Japan.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                             PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp Spc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1.
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  Score 1062; DB 4;
Pred. No. 6e-94;
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0106508; P:proteolysis and peptidolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Gene Analysis of Anticoagulation Factors in Japanese Thrombotic Patients. Genetic Background of Thrombophilia in Japan."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M.,

Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M.,

Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M.,
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[1]
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Mammalia; Eutheria;
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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                                                                                          CAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIH
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SEQUENCE
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Xenopus laevis (African clawed frog)
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                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                            "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Generation and initial analysis of more than 15,000 and mouse cDNA sequences "; ^{\prime\prime}
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Submitted (JUL-2003) to the
EMBL; BC054968; AAH54968.1;
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Xinoshita S., Iida H., Inoue S., Watamare

Xinoshita S., Iida H., Inoue S., Watamare

Xinoshita S., Iida H., Inoue S., Watamare

Xinoshita S., Iida H., Inoue S., Watamare

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01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSFLEETRHSSTERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVVKITIHPEYRSDTNDNDIALLRLVQPVVYNKYILPICLPSLDLAENTLMVNGTVVVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CVNAECKDGIGREDCICNEGWEGRLCGYEVVYSNCSLNNGGCSHFCTQPMNSTRRVC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWG----REDEKALNESSVLSYIQIPVVSHNQCAETLNDRLSDNMLCAGRLGHIQDACYG
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Pred. No. 1.9e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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smatches 112; Indels
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Best Local Similarity
Matches 291; Conserva
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R Pram; Pr0089; trypsin; 1.

R Prints; PR00001; GLABLOOD.

R PRINTS; PR00001; GLABLOOD.

R SWART; SM00069; GLA; 1.

SWART; SM00069; GLA; 1.

SWART; SM00020; Tryp_SPC; 1.

SWART; SM00020; Tryp_SPC; 1.

R PROSITE; PS00010; ASX HYDBOXYL; 1.

R PROSITE; PS001187; EGF CA; 1.

R PROSITE; PS01187; EGF CA; 1.

R PROSITE; PS001187; EGF CA; 1.

R PROSITE; PS001187; EGF CA; 1.

R PROSITE; PS001187; EGF CA; 1.

R PROSITE; PS001187; EGF CA; 1.

R PROSITE; PS00111; GLU CARBOXYLATION; 1.

R PROSITE; PS00011; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:9771; Proc.

GO; GO:00055976; C:extracellular; IEA.
GO; GO:00055976; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:calcymortypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
GO; GO:0006509; P:proteolysis and peptidolysis; IEA
InterPro; IPR001254; Peptidase
GIA.
R InterPro; IPR001254; Peptidase
GIA.
R InterPro; IPR001314; Peptidase
GIA.
R InterPro; IPR001344; VitK_dep_GIA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anticoagulant protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF318182; AAK07918.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL
-!- SIMILARITY: BELONGS TO PEPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
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                          APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQV--DPRLIDGKMTRR
                                                                                      SPCCGHGTCIDGIGSPSCSCDXGWEGKFCQQELRFQDCRVNNGGCLHYCLEESNGRRCAC
                                                                                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                          ANSTLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                                                ANSFLEENRPGSLERECMEETCDLEEAQETFQNVEDTLAFWIKYFDGDQCSAPPLDHQCD
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                            70.1%;
69.6%;
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55;
                                                                                                                                                                                                                                                                                                           Score 1629; DB 11,
; Pred. No. 4.7e-148;
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                                                                                              161
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Q804X5;
Q1-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IRR009003; Cys Ser trypsin.
InterPro; IPR000742; EGF 2.
InterPro; IPR000881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR0052383; GLA blood.
InterPro; IPR0052310; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,

Tuddenham E.G.D., McVey J.H.;

Tuddenham E.G.D., McVey J.H.;

"Comparative sequence analysis and molecular evolution of blood

"Comparative sequence from Gallus gallus and Fugu rubripes.";

Submitted (Jan-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, N4465270; AAO33365.1; -:
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
           PROSITE;
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PROSITE;
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                                                                                                                                                                                                                                                                                            Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
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                                                                                                                                                                                                                                          SMART; SM00179;
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000152; Asx_hydroxyl
                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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GO:0005509; F:calcium ion binding; IEA.
GO:0004263; F:chymotrypsin activity; IEA.
GO:0016787; F:hydrolase activity; IEA.
GO:0003808; F:protein C (activated) activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0004295; F:trypsin activity; IBA. GO:0006508; P:proteolysis and peptid
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                                SM00181; BGF; 2.

SM00179; BGF CA; 1.

SM00069; GLA; 1.

SM00020; Tryp SPc; 1.

E; PS00010; ASX HYDROXYL; 1.

E; PS00012; BGF 1; 1.

E; PS01186; BGF 2; 2.

E; PS01187; BGF CA; 1.

E; PS00111; GLU CARBOXYLATION; 1.
                                                                                                                                                                                     SM00020;
                                                                                                                                                                                                                                                                  SM00181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001254; Peptidase S1.
IPR001314; Peptidase S1A.
IPR000294; VitK_dep_GLA.
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3 (TrEMBLrel. 24,
3 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolysis and peptidolysis; IEA
52; Asx hydroxyl S.
        TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Veognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25, Last annotation update) precursor (EC 3.4.21.69).
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Last
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                                                                                           Q91WN8;
Q91WN8;
01-DEC-2001
01-DEC-2001
01-OCT-2003
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                     PROC.
                                    Mus musculus (Mouse)
                                                                      Similar to protein
                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                                                                                                                                             GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                  KEVLIHPNYSKSTIDNDIALLHLAQPAIFSQTIVPICLPDSGLABRELTQVGQETVVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
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                                                                                                                                                                                                                                                        GGPMVTSFRGTWFLVGLVSWGEGCGRLHNYGIYTKVSRYLDWIHSHIRGEEASLENQVP
                                                                                                                                                                                                                                                                                                                              GYRS---
                                                                                                                                                                                                                                                                                                                                                       GYHSSREKEAKRNRTFYLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                    Metazoa; Chordata;
                                                                        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
protein C.
                                                                                                                                                                   PRELIMINARY;
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 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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MGD; MGI:97771; Proc.

RGO; GO:00055076; C:extracellular; IEA.
RGO; GO:00055076; F:calcium ion binding; IEA.
RGO; GO:00055079; F:calcium ion binding; IEA.
RGO; GO:0004283; F:chymotrypsin activity; IEA.
RGO; GO:0004283; F:chymotrypsin activity; IEA.
RGO; GO:0006508; F:trypsin activity; IEA.
RGO; RGO:0006508; F:proteolygis and peptidolysis; IEA.
RGO; RGO:0006508; F:proteolygis and peptidolysis; IEA.
RGO; RGO:0006508; P:RROO152; Asx_hydroxyl_S.
RINterPro; IPR00152; Asx_hydroxyl_S.
RINterPro; IPR001881; EGF_Ca.
RINterPro; IPR006209; EGF_Like.
RINterPro; IPR001254; Peptidase_S1.
RINterPro; IPR001254; Peptidase_S1A.
RINterPro; IPR001254; Peptidase_S1A.
RINterPro; IPR001294; VitK_dep_GLA.
R InterPro; IPR001294; VitK_dep_GLA.
R Pfam. PR00164: 101: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMOOLT9; ESP CA; 1.

SMART; SMOOLT9; ESP CA; 1.

SMART; SMOOLT9; ESP CA; 1.

SMART; SMOOLT9; ESP C; 1.

PROSITE; PSOOLT0; ASX HYDROXYL; 1.

PROSITE; PSOOLT16; ESP 2; 2.

PROSITE; PSOOLT16; ESP C; 1.

PROSITE; PSOOLT16; ESP C; 1.

PROSITE; PSOOLT16; GLU CARBOXYLATION; 1.

PROSITE; PSOOLT14; GLU CARBOXYLATION; 1.

PROSITE; PSOOLT14; TRYPSIN DOM; 1.

PROSITE; PSOOLT14; TRYPSIN HIS; 1.

PROSITE; PSOOLT15; TRYPSIN SER; 1.

EGF-11ke domain; Hydrolase; Protease; S
SEQUENCE 460 AA; 51818 MW; 0117F26E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 292;
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Best Local
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-I-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; EC013896; AAH13896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLCOD.
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                           359 DSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKS
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                                                                        SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                                                     DIKETLVHPNYTRSSSDNDIALLRLAQPATLSKTIVPICLPNNGLAQ-ELTQAGQETVVT
                                                                                                                                                                                                          DIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQBTLVT
                                                                                                                                                                                                                                                                 APGYELADDHMRCKSTVNFPCGKLGRWIEKKRKILKRDT-DLEDELEPDPRIVNGTLTKQ
                                                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKEMEKKRSHLKRDTEDQEDQV--DPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPCCGHGTCIDGIGSFSCSCDKGWEGKFCQQELRFQDCRVNNGGCLHYCLEESNGRRCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSPILEEMRPGSLERECMERICDFERAGEIFONVEDTLAFWIKYFDGDQCSAPPLDHQCD 101
                                                                                                 Conservative
70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55;
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Pred. No. 1.2e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   otease; Serine protease.
0117F26E68FCC274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 460;
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238 220

298 280

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Title:
Perfect score;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
bisting first 45 summaries
                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
4: sp_human:*
5: sp_invert
6: sp_manma
7: sp_mbc:*
8: sp_orga
9: sp_bha*
10: sp_p
11: sp_r
12: sp_r
13: sp_r
14: sp
15: sp
15: sp
16: sp
17:
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2324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                                                                                      sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                        sp_organelle:*
sp_phage:*
   sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                               sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                           1017041
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	q Query Match Length	DB	Ħ	Description
1	1894.5	81.5	456	6	Q9TTRO	Q9ttr0 canis famil
2	1635	70.4	460	11	091WN8	Q91wn8 mus musculu
ω	1629	70.1	460	11	Q99PC6	Q99pc6 mus musculu
4	1143.5	49.2	433	13	Q804X5	Q804x5 gallus gall
رب ر	1134.5	48.8	455	13	Q7SY86	Q7sy86 xenopus lae
on.	1063	45.7	195	4	Q8J008	Q8j008 homo sapien
7	1062	45.7	195	4	Q8J007	Q8j007 homo sapien
80	1059	45.6	195	4	Q8J006	Q8]006 homo sapien
9	1059	45.6	195	4	Q8IXB4	Q8ixb4 homo sapien
10	975.5	42.0	434	13	Q7T3B6	Q7t3b6 brachydanio
11	927	39.9	211	4	Q8J009	Q8j009 homo sapien
12	818.5	35.2	482	11	Q63207	Q63207 rattus norv
13	799.5	34.4	425	13	Q804X7	Q804x7 gallus gall
14	794	34.2	481	11	088947	088947 mus musculu
15	793	34.1	481	11	054740	enm (
16	793	34.1	481	11	Q99L32	Q99132 mus musculu

44	43	42	41	40	39	38	37	36	35	34	ω <b>3</b>	32	31	ω (9)	29	28	27	26	25	24	23	22	21	20	19	18	17
456 440.5	457	470	475	477.5	479.5	512	523	525	565.5	565.5	671.5	688.5	703	711.5	718	734.5	739.5	740	743	749.5	772	773	775	781	784	787	788
19.6	19.7	20.2	20.4	20.5	20.6		22.5		24.3	24.3	28.9	29.6	30.2	30.6	30.9	31.6	31.8	31.8	32.0	32.3	33.2	33.3	33.3	33.6	33.7	33.9	33.9
680 1379	540	399	681	653	340	607	612	809	622	524	474	537	503	443	461	430	471	461	442	441	446	469	475	679	433	433	446
ហហ	13	11	13	11	Ľ	13	13	13	4	13	13	13	13	13	6	13	13	6	13	13	11	6	13	4	13	13	11
Q868H5 Q9V4N6	Q800Y7	Q9CQW3	Q7ZT70	Q8VCS4	Q80Y26	Q91001	Q804W7	Q9PTW7	Q7Z7P3	Q7SXH8	<b>О</b> ВЛНСВ	Q804W8	Q8AYE4	овлнс9	Q95ND6	Q804X0	Q804X6	Q95ND7	Q804X1	Q804X2	Q61109	Q9GMD9	Q804W9	Q9 6 P Q 8	Q8JHD0	Q90YK1	Q8K3U6
Q9v4n6 drosophila			Q7zt70 lampetra ja	_	Q80y26 mus musculu	Q91001 gallus gall		Q9ptw7 struthio ca	-5	Q7sxh8 brachydanio				Q8jhc9 brachydanio			Q804x6 gallus gall	Q95nd7 pan troglod			Q61109 mus musculu		ဖ	$\sim$		Q90yk1 brachydanio	

### ALIGNMENTS

	DR DR CCC	R R R R R R	RRARRA	58888		RESULT Q9TTRO ID Q
GO:000 GO:000 GO:000 GO:000 erPro; erPro;	"Analysis of can Anim, Genet. 30: -!- SIMILARITY: EMBL; AJ001979; HSSP; P04070; LA GO; GO:0005576; GO; GO:0005509;	Mamm. Genome 10:13 [2] SEQUENCE FROM N.A. MEDLINE=99371952; Leeb T., Pfeiffer	SEQUENCE FRO SEQUENCE FRO Leeb T., Kop Brenig B.; "Molecular o	PROC. Canis familiaris (Do Canis familiaris (Do Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9615;	01-MAY-2000 (TrEMBLE 01-MAY-2000 (TrEMBLE 01-OCT-2003 (TrEMBLE Protein C precursor.	OPTIRO
190	"Analysis of Canine protein tyens panim. Genet. 30:237-238 (1999)!- SIMILARITY: BELONGS TO PEPTIDASE EMBL; AJ001979; CAA05126.1; HSSP; P04070; LAUT. GO: GO:0005576; C:extracellular; IEA GO: GO:0005579; F:calcium ion bindin	PROCEIL C GENE: 7 Mamm. Genome 10:135-139(1999). [2] [2] [2] [3] [2] [4] [5] [6] [6] [7] [7] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Leeb T., Kopp T., Deppe A., Breathering B.;  Whelecular characterization and	(Dc oa; ia;	(TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 25, ecursor.	PRELIMINARY;
Frohymotrypain activity; IEA. Frephtidase activity; IEA. Fritypsin activity; IEA. Proteolysis and peptidolysis; IEA. 152; Asx hydroxyl S. 003; Cys Ser trypsin. 881; EGF Ca.	"ARALYSIS OF CARLINE PROCEDIT C GENE POLYMOLPHISMS: , Anim. Genet. 30:237-238 (1999)	PROCELL C General Common Mamm. Genome 10:135-139 (1999).  [2] [2] [3] [8] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	, Breen M., Matis U., Brunnberg n and chromosomal assignment of	og). Chordata; Craniata; Vertebrata; Eutel Carnivora; Fissipedia; Canidae; Canis	, Created) , Last sequence update) , Last annotation update)	PRT; 456 AA.
			erg L., of the canine	Buteleostomi; Canis.		

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PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Elood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
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321 RVSGWGQLLDRGATA-----LELMSIEVPRLMTQDCLEHAKHSSNTPKITENMFCAGYMD 375
                                          296 LVTGWGYHSSREKEAKRNRTFVLNFIKIFVVPHNECSEVMSN-----MVSENMLCAGILG 350
                                                                                     262 OVRRVTQVIMPDKYIRGKINHDIALLRLHRPVTFTDYVVPLCLPEKSFSENTLARI-RFS 320
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                                                                                                                                                                                                                                                                                                                                                              --CQNGGTCQDHLKSYVCFCLLDFEGRNCEKSKNEQLICANENGDCDQYCRDHVGTKRTC 153
                                                                                                                                                                                                                                                                                                                                                                                                      STCCGHGTCIDGIGSESCDCRSGWEGRECQREVS-FINCSLDNGGCTHYCLEEVGWRR-C
                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSILEELWPGSLERECNEEQCSFEEAREIFKSPERTKQFWIVYSDGDQCASNP-----
                                                                                                                                                                            GECPWOAV-LKINGLLLCGAVLLDARWIVTAAHCFDNIRYWGNITVVMGEHDFSEKDGDE 261
                                                                                                                    LDLDIKEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLFDSGLABRELNQAGQET 295
                                                                                                                                                                                                                  GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                                                                    SCHEDYTLOPDEVSCKPKVEYPCGR-IPVVEKRNSSSRQG-----RIVGGNVCPK 202
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Pred. No. 2.4e-53;
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
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N-LINKED (GLCNAC. ..) (POTENTIAL)
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Qy 351 DRQDACEGDSGGPMVASFHGTWFLVGLVSNGEGCGLLHNYGVYTKVSRYLDWTHGHIRDK 410
bb 376 GTKDACKGDSGGPHATHYHGTWYLTGVVSNGEGCAAIGHIGVYTRVSQYIDWLVRHWDSK 435
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Search completed: June 2, 2004, 16:56:13
Job time : 38 secs

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Castellino F. murine blood

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                                                                                                                               GSKDACKGDSGGPHATRFRGTWFLTGVVSWGEGCAAAGHFGIYTRVSRYTAWLRQLMGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPCQNGGSCEDQLRSYICFCPDGFEGRNCETDKQSQLICANDNGGCEQYCGADPGAGRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQRE-VSFLNCSLDNGGCTHYCLEEVG-WRRC 118
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                                                                                                                                                                   DRODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIH---GH
                                                                                                                                                                                                            AVSGWGQLLERGVTARK---
                                                                                                                                                                                                                                                  LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN-----MVSENMLCAGILG
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EGF-LIKE 2.
SERINE PROTEASE.
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Pred. No. 3.
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N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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703E1FE0636F7F10 CRC64;
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                             PRT;
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                               446 AA
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            InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR009003; Cys_Ser_trypsIn.
InterPro; IPR0090742; EGF_2.
InterPro; IPR001488] EGF_GA.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_like.
InterPro; IPR0062383; GLA_blood.
InterPro; IPR0012383; GLA_blood.
InterPro; IPR001214; Peptidase_S1A.
InterPro; IPR001214; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GIA.
            PROSITE; PRODUCT; PAPROSITE; PRODUCT; PAPROSITE; PSOUDCE; PAPROSITE; PSOUDCE; PROSITE; PSOUDCE; PROSITE; PSOUDCE; PAPROSITE; PSOUDCE; PROSITE; PSOUDCE; PROSITE; PSOUDCE; PROSITE; PSOUDCE; PROSITE; PSOUDCE; PROSITE; PSOUDCE; PROSITE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOUDCE; PSOU
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Ol-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a linear temporal.
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Mammalia; Eutheria;
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--- TISSUE SPECIFICITY: Plasma.

--- PTM: The vitamin K-dependent, enzymatic carboxylat glutamate residues allows the modified protein to similarity).

--- SIMILARITY: Belongs to peptidase family Sl.

---- SIMILARITY: Contains 2 EGF-like domains.
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MEDLINE=97127167; PubMed=8972017;
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                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U66079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide structure and characterization coagulation factor VII gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Idusogie E., Rosen E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                              Pfam; PF00594; gla; l.
Pfam; PF00089; trypsin; l.
                                                                                                                                                                                                                                                                                                                  Pfam; PP00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:109325;
                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                        PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Circulates in the blood in a zymogen form. Factor VII converted to factor VIIa by factor XA, factor XIIa, factor IXa, thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor X by limited proteolysis. Factor VIIa will also convert factor IX factor IXa in the presence of tissue factor and calcium (By factor IXa in the presence of tissue factor and calcium (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity). CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Heterodimer of a light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             form factor Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                        F; SM00179; EGF_CA; 1.
C; SM00169; GLA; 1.
C; SM00069; GLA; 1.
CTE; PS00010; ASX_HYDROXYL; 1.
CTE; PS00012; EGF_1; 1.
CTE; PS01016; EGF_2; FALSE_NEG.
CTE; PS50026; EGF_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P08709;
                                                                                                                                                                                                                PR00722; CHYMOTRYPSIN PR00010; EGFBLOOD. PR00001; GLABLOOD.
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EGF_CA; 1.
GLU_CARBOXYLATION; 1.
TRYPSIN_DOM; 1.
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                                                                                                                                                                                                                                                  P22457;
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01-AUG-1991
10-OCT-2003
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of single-nucleotide polymorphisms in
                                                                                                                                                                                                                          Coagulation
  SEQUENCE
                                                                                                                                                                                                     accelerator)
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itat. Suppl. 1:S189-S191(1998).
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d L., Rolfe A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFLNCSLDNGGCTHYCLEEVGWRR-C
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(Rel. 42, L
factor VII
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38.8%;
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Last annotation updat
I (EC 3.4.21.21) (Seru
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3.4.21.21) (Serum:
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Pred. No. 2.4e-54
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araman N., 1
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                                                                                                                                                                                                                                  prothrombin conversion
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MEDLINE-89213999; PubMed-3149637;
Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.,
"A new trisaccharide sugar chain linked to a serine residue
"A new trisaccharide sugar chain linked to a serine residue
blood coagulation factors VII and IX.";
                                                                                                PROSITE; PS001186; E
PROSITE; PS001076; E
PROSITE; PS001107; G
PROSITE; PS00011; G
PROSITE; PS000134; T
PROSITE; PS001134; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."; Adv. Exp. Med. Biol. 281:121-131(1990).

-i- FUNCTION: Circulates in the blood in a zymogen form. Factor VII is converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor X by limited proteolysis. Factor VIIa will also convert factor IX to factor IXa in the presence of tissue factor and calcium.

-i- CATALYTIC ACTIVITY: Hydrolyzes one Arg- |-ile bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence."
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Iwanaga S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            form factor Xa.

-i- SUBUNIT: Heterodimer of a light chain and a heavy chain linked a disulfide bond.

-i- TISSUE SPECIFICITY: Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.
-i- SMILARITY: Belongs to peptidase family S1.
-i- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE OF CARBOHYDRATE ON SER-52.
                                                                                                                                                                                                                                                                                                                                                        InterPro; II
InterPro; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bovine factor VII. Its purification and complete amino
                                          Liver; Pl
EGF-like
                                                                                                                                                                                                                              SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91344709; PubMed=2129367;
Iwanaga S., Nishimura H., Kawabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE OF CARBOHYDRATE ON SER-52.
                                                                                                                                                                                     PROSITE; PS00010;
PROSITE; PS00022;
                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                 Ptam;
                                                                                                                                                                                                                                                                                                                                             InterPro; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                   PROSITE; PS00135;
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                                              "TTE; PS00101; GLAFLOD
"TE; PS00101; ASX HYDROXYL; 1.
"TE; PS00101; ASX HYDROXYL; 1.
"TE; PS00118; EGF_2; 2.
"PS0118; EGF_3; 1.
"S0011; GLU CARBOXYLATION; 1.
"S00011; GLU CARBOXYLATION; 1.
"134; TRYPSIN DOM; 1.
"134; TRYPSIN LHIS; 1.
"15; TRYPSIN SER; 1.
"TE protease; B1"
"Temin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A31979; KFB07
                                                                                                                                                                                                                                                                                 PF00594; gla; 1.
PF00089; trypsin; 1.
S: PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P08709;
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IPR001438;
IPR006209;
IPR002383;
                                          domain;
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IPR000742; EGF_2.
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                                                                                                                                                                                                                                                                                                                                               PR000294;
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 ; Repeat.
152
407
35
                                                                                                                                                                                                                                                                                                                                             Peptidase_S1.
Peptidase_S1A.
VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                        EGF_Ca.
EGF_II.
EGF_like.
GLA_blood.
                                                       ē; Blood coagulation; Zymogen; Glycoprotein;
Calcium-binding; Gamma-carboxyglutamic acid
               FACTOR VII LIGHT CHAIN FACTOR VII HEAVY CHAIN
    GLA-RICH
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(Xyl2-Glc)
epidermal c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=91344709; PubMed=2129367; Ivenaka S., Kisiel W., Hase S., Ikenaka Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka Wa new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z. Adv. Exp. Med. Biol. 281:121-131(1990).
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Nishimura H., Kawabata S., Kisiel W.,
Shimonishi Y., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosylations at serine residues 52 and 60 and effects directed mutagenesis of serine 52 to alanine.";
J. Biol. Chem. 266:11051-11057(1991).
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Bjoern S., Foster D.C., Thim L., Wiberg F.C.,
Komiyama Y., Pedersen A.H., Kisiel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor VIIa from plasma and tra
Biochemistry 27:7785-7793(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence and posttranslational modifications of human
factor VIIa from plasma and transfected baby hamster kidney cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thim L.,
          Marchetti G., Patracchini P., Gemmati D., Derosa V., Pinot Rodorigo G., Casonato A., Girolami A., Bernardi P.; "Detection of two missense mutations and characterization polymorphism in the factor VII gene (F7)."; Hum. Genet. 89:497-502(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96175641; PubMed=8598903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE OF CARBOHYDRATE ON SER-112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human plasma and recombinant factor VII. Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES
                                                                                  VARIANTS GLN-364 AND PHE-370.
WRDLINE=92340074; PubMed=1634227;
                                                                                                                                             maie.
                                                                                                                                                      "Purification and characterization of factor VII 304-Gln: molecule with reduced activity isolated from a clinically
                                                                                                                                                                                       O'Brien D.P., Gale K.M., Ande
Meade T.W., Tuddenham E.G.D.;
                                                                                                                                                                                                                                                                                                     Drakenberg T.;
                                                                                                                                                                                                                                                                                                                      Muranyi A., Finn
                                                                                                                                                                                                                                                                                                                                   MEDLINE=98367502;
                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 105-145
                                                                                                                                                                                                                                                                                                                                                                              J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                            zhang B., St Charles R., Tulinsky A.;
"Structure of extracellular tissue factor
inhibited with a BPTI mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99126538; PubMed=9925787;
                                                                                                                                                                                                                 MEDLINE=91300046; PubMed=2070047;
                                                                                                                                                                                                                                                             Biochemistry 37:10605-10615(1998)
                                                                                                                               Blood 78:132-140(1991)
                                                                                                                                                                                                                                    VARIANT GLN-364.
                                                                                                                                                                                                                                                                                       Solution structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                 Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth factor-like domain of human factors VII and IX and and bovine protein Z.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ation of a disaccharide (Xyl-Glc) and a trisaccharide O-glycosidically linked to a serine residue in the fi
                                                                                                                                                                                                                                                                                                                                                                               285:2089-2104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264:20320-20325(1989).
                                                                                                                                                                                                                                                                                                                      B.E., Gippert G.P.,
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                                                                                                                                                                                                                                                                                                                                      PubMed=9692950;
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                                                                                                                                                                                                                                                                                          the N-terminal EGF-like
                                                                                                                                                                                                    Anderson J.S., McVey J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SER-112 AND SER-120
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    Roberts H.R., Blajchman M., Monroe D.M., High K.A.; "Severe factor VII deficiency caused by mutations abolishing cleavage site for activation and altering binding to tissue f Blood 83:3524-3535(1994).
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Bernardi F., Cascaman G., Redealli R.,
Rodeghiero F., Marchetti G.,
"Topologically equivalent mutations ca
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"Ala244Val is a common, probably ancient
deficiency in Moroccan and Iranian Jews."
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Lunghi B., Rodeghiero F., Marchetti G.;
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Brenner B., Paz M., Luder A.S., Blau
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    the signal sequence deficiency.";
                                 "Factor VII Morioka
                                             Sakuragawa N.;
                                                              Ozawa T., Takikawa Y.,
                                                                            MEDLINE=98235713; PubMed=9576180;
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                                                                                                                MEDILINE=0,2007..., Grant F.J., Haldeman B.A., Grant F.J., Grant F.J., Haldeman B.A., Grant F.J., Grant F.J., Haldeman B.A., Grant F.J., Murray M.J.; Hagen F.S., Murray M.J.; Hagen coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding for human factor VII, a "Nucleotide sequence of the gene coding fo
                                                             SEQUENCE PROM N.A., AND Rieder M.J., Armel T.Z., Poel C.L., Toth E.J., Yi
                                                                                                                                                                                                                                                                                                                Davie E.W.;
             SEQUENCE
                                              Submitted
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=87260948; PubMed=3037537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFLEEMKQGNIERECNEERCSKEEAREAFEDNEKTEEFWNIYUDGDQCSSNP-
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                                                                                                                                                                                                                                                                             LNEDFILTAAHCINQSKEIKVVVGEVDREKEEHSETTHTAEKIFVHSKYIAETYDNDIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CHYGGQCKDGLGSYTCSCLDGYQGKNCEFVIP-KYCKINNGDCEQFCSIKKSVQKDVV
                                                                                                                                                                              IKLKEPIOFSEYVVPACLPQADFANEVLMNQ--KSGMVSGFGREFEAGRLSKR----
                                                                                                                                                                                                                            LHLAQPATLSQTIVPICLPDSGLAEREL-NQAGQETLVTGWGYHSSREKEAKRNRTFVLN 319
                                                                                                                                                                                                                                                                                                                                                                    EEVFTTTTES PTPP PRNGSSITD PNVDTRIVGGDECRPGECEWQAVLINEKGEEFCGGTI
                                                                                       VLEVPYVDRSTCKQSTNFAITENMFCAGYETEQKDACQGDSGGPHVTRYKDTYFVTGIVS
                                                                                                                                     FIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVS
WGEGCARKGKYGVYTKLSRFLRWVRTVMRQK 475
                                         WGEGCGLLHNYGVYTKVSRYLDWIHGHIRDK 410
                                                                                                                                                                                                                                                                                                                        IHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIAL
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01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum conversion accelerator) (Eptacog alfa).
                                                                                                                                                                                                                                                                                                                                                                                                                  FA7_HUMAN
P08709; Q14339;
                                                       MEDLINE=86205965; PubMed=3486420;
Hagen F.S., Gray C.L., O'Hara P.J., Gra
Woodbury R.G., Hart C.E., Insley M.Y.,
                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                            NCBI_TaxID=9606;
"Characterization of a cDNA coding for human fact
Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986)
                                                                                                                                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                      Primates;
                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                              Grant F.J., Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                 466
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                       factor VII.";
                                                                   , Saari G.C.
M., Kurachi
                                                                                                                                                                                                                                                                                                                                   prothrombin
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Similarity

61-466,

AND POST-TRANSLATIONAL MODIFICATIONS

AND VARIANTS THR-352; GLN-413 AND LYS-445. T.Z., Carrington D.P., Chung M.-W., Lee K.L., Yi Q., Nickerson D.A.; ) to the EMBL/GenBank/DDBJ databases.

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RESULT 12
FA10_CHICK
ID FA10_C
AC P25155
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVS-FLNCSLDNGGCTHYCLEEVGWRR-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFLEELRPGSLERECKEELCSFEEAREVFQSTERTKQFWITYNDGDQCASNP-----
                                                                                                                                                   YLDGSKDACKGDSGGPHATSYHGTWYLTGVVSWGEGCAAVGHVGVYTRVSRYTEWLSRLM
                                                                                                                                                                                  ILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHI
                                                                                                                                                                                                                                            LVTGWG----YHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM-----SNMVSENMLCAG
                                                                                                                                                                                                                                                                           QVRHVAQLIMPDKYVPGKTDHDIALLRLLQPAALTNNVVPLCLPERNFSESTLATI-RFS
                                                                                                                                                                                                                                                                                                       LDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET
                                                                                                                                                                                                                                                                                                                                     GECPWQAALMNG-STLLCGGSLLDTHWVVSAAHCFDKLSSLRNLTIVLGEHDLSEHBGDE
                                                                                                                                                                                                                                                                                                                                                                GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDE---SKKLLVRLGEYDLRRWBKWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         --CONGGSCEDQIOSYICFCLADFEGRNCEKNKNDQLICMYENGGCEQYCSDHVGSQRSC
                                                                                                                        RDK 410
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                   STANDARD;
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GAMMA-CARBOXYGLUTAMIC ACID.
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Pred. No. 7.3e-56;
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N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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SIMILARITY.
BSTRATE (BY SIMILARITY).
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                                                                                                                                                                                                                 -LMAIDVPRLMTQDCVEQSEHKPGSPEVTGNMFCAG
                   475
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                                                                                                                                                                                                                     370
         01-MAY-1992
01-MAY-1992
15-MAR-2004
Coagulation 1
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FEBS Le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogasawara T., Nagai Y.;
"Primary structure of the virus activating protease from chick embryo. Its identity with the blood clotting factor Xa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Chorioallantoic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Allantoic fluid;
MEDLINE=91065352; PubMed=2174359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91257322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gotoh B., Ogasawara T., Toyoda T., Inocencio N.M., Hamaguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 41-55 AND 241-261.
                   InterPro; IPRO
Pfam; PF00008;
                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                          bet ween
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determinant of viral tropism in chick embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                 InterPro;
                                                                                                                                                          InterPro;
                                                                                                                                                                        InterPro;
                                                                                                                                                                                        MEROPS;
                                                                             interPro;
                                                                                               InterPro;
                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                by the excision of two Arg residues and are held together by 1 on more disulfide bonds.

TISSUE SPECIFICITY: Liver and chorioallantoic membrane.

PIM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.

PIM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE EXTRINSIC PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
FUNCTION: VAP cleaves the fusion proteins of Sendai virus, NDV, and influenza virus a at a specific single arginine-containing site, and plays a key role in the viral spreading in the allantoic
                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by mon-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \text{Arg-}|\text{-Ile} bonds in prothrombin to form thrombin. SUBUNIT: The two chains are formed from a single-chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sac.
CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endoprotease homologous to the blood clotting
                                                                                                                                                                                                                     ; D00844; BAA
S15838; EXCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lett. 283:281-285(1991).
                                                                                                                                                                                                      P00742;
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                               o; IPR000152; Asx hydroxyl S.
o; IPR009003; Cys Ser_trypsin.
o; IPR000742; EGF 2.
o; IPR00181; EGF Ca.
o; IPR01438; EGF II.
o; IPR06209; EGF like.
o; IPR005209; EGF Like.
o; IPR001383; GLA-blood.
o; IPR001254; Peptidase S1.
o; IPR001314; Peptidase S1A.
o; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                      S01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9:4189-4195(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harada A., Hayashi Y., Wada K., Asaka J.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 43, Last annotation update)
factor X precursor (EC 3.4.21.6) (Stuart factor)
                                                                                                                                                                                                      IHCG.
                                                                                                                                                                                                                                    BAA00724.1;
      EGF;
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factor X

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RESULT 11
FA7_RABIT
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Best Local Similarity
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PDB; 1NFY; 25-FEB-03.
PDB; 1NFY; 25-FEB-03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; TAS. GO; GO:0003804; F:blood coagulation f GO; GO:0007596; P:blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:3528; F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlycoSuiteDB; P00742; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.216; -.
                                  01-FEB-1996
15-JUL-1998
10-OCT-2003
                     Coagulation factor VII precursor
                                                                          P98139; P79224;
                                                                                             FA7 RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227600; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA
                                                                                                                                                                   CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP
                                                                                                                                                                                                                          PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEG
                                                                                                                                                                                                                                                       PVVPHNECSEVNSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG
                                                                                                                                                                                                                                                                                    TPITFRMNVAPACLFERDWAESTL--MTQKTGIVSGFGRTHEKGRQSTR-----KKMLEV
                                                                                                                                                                                                                                                                                                              QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI
                                                                                                                                                                                                                                                                                                                                            YILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLK
                                                                                                                                                                                                                                                                                                                                                                       WVLTAAHCWDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                    PTENEFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- CONOGRCKOGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC
       (Rel. 36, Last Beque... (Rel. 42, Last annotation update)

(Rel. 42, Last annotation update)

The recursor (EC 3.4.21.21) (Serum prothrombin)
                                                               (Rel. 33, Created)
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                                                                                              STANDARD;
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%; Pred. No. 2.3e-56;
87; Mismatches 151;
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  SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01186; EGF 3; 1.

PROSITE; PS00026; EGF 3; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS000134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruiz S.R., Blajchman M.A., Clarke B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to peptidase family $1.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>-</u>
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HSSP; P08709; 1FAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement
                                                                                                                                SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                  Pfam; PF00594; gla;
                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl_S
                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.215;
                                                                                                                                                         PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                         PRINTS; PRO0010; EGFBLOOD.
                                                                                                                                                                                                                                    Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                 InterPro; IPR001314; Peptidase_S1A
InterPro; IPR000294; VitK_dep_GLA.
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                                                                                                                                                                                                                                                                                                                                                                 interPro;
                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a disulfide bond (By similarity). TISSUE SPECIFICITY: Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
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                                                                                                                                                                                                                                                                                                      ; IPR001881; EGF_Ca.
; IPR001438; EGF_II.
; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                           IPR001254; Peptidase_S1
                                                                                                                                                                                                                                                                                             IPR002383; GLA_blood.
                                                                                                                                                                                                                                                                                                                                                   IPR009003; Cys_Ser_trypsin.
IPR000742; EGF_2.
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conversion accelerator).

맑 S 밁 S 용 S

> Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases FUNCTION: Circulates in the blood in a zymogen form. Factor VII is converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or SUBUNIT: Heterodimer of a light chain and a heavy chain linked CATALYTIC ACTIVITY: Hydrolyzes one Arg- | - Ile bond in factor X to by limited proteolysis. Factor VIIa will also convert factor IX to and calcium ions, factor VIIa then converts factor X to factor Xa thrombin by minor proteolysis. In the presence of tissue factor factor IXa in the presence of tissue factor and calcium (By

PTM: The vitamin K-dependent, enzymatic carboxylation of glutamate residues allows the modified protein to bind ca calcium some (By

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modified and this statement is not removed

is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/

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                                                                    Query Match
Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                                 PEAM: PF00594; gla; 1.

PEAM: PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00702; GLABLOOD.

SMART; SM00179; BGF CA; 1.

SMART; SM00020; GLA; 1.

SMART; SM00020; Tryp Spc; 1.

SMART; SM00020; Tryp Spc; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS01186; EGF 1; 1.

PROSITE; PS01186; EGF 3; 1.

PROSITE; PS00187; EGF GA; 1.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS00011; GLU CARBOXYLATION; 1.

PROSITE; PS000134; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA blood.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; VitK_dep_GLA.
InterPro; IPR001294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                              DOMAIN
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                                                                    Local Similarity
les 172; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 1MHF; 15-MAY-97.
; 1IOD; 21-JAN-03.
; 1KIG; 28-OCT-98.
                                                                                                                   RES
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  51
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  SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQ---REVSFLNCSLDNGGCTHYCLEEVGWRR
                                              ANSFLEELRHSSLERECIEEICDEBEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
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15-MAY-97.
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41
183
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234
476
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234
275
275
418
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                                                                     Conservative
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                                                                                                                                                                                                                                                                      23
180
192
233
492
492
                                                                                34.8%;
                                                                       72;
                                                                                                                    GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                       SERINE PROTEASB.
CHARGB RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                     Score 809.5; DB 1
Pred. No. 2.1e-56;
2; Mismatches 150
                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
MAY BE REMOVED BUT IS NOT NECESSARY FOR
ACTIVATION.
                                                                                                                                                                                                                                                                                                         FACTOR X HEAVY CHAIN.
                                                                                                                                                                                                                                                  CALCIUM-BINDING (POTENTIAL)
                                                                                             DB 1;
                                                                         150;
                                                                         Indels
                                                                                             Length
                                                                                                492;
                                                                         73;
                             ---ECHPCL
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21-JUL-1986 (Rel
01-OCT-1989 (Rel
10-OCT-2003 (Rel
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coagulation
MEDLINE-2388257; PubMed=12477932;
MEDLINE-2388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                           Rieder M.J., Armel T.
Ozuna M., Poel C.L.,
Submitted (APR-2002)
                                                                                                                                                                                                                                                                                                        MEDINE-87026600; PubMed=3768336;
Leyrus S.P., Foster D.C., Kurachi K., Davie E.W.;
"Gene for human factor X: a blood coagulation factor whose organization is essentially identical with that of factor I
                                                                                                                                                                                                                                                                                                                                                                                                      Messier T.L., Pittman D.D., Long "Cloning and expression in COS-1 human coagulation factor X."; Gene 99:291-294(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FA10_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91216473; PubMed=1902434;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Biochemistry 25:5098-5102(1986).
                                                                                                                                                                                                                                                                                             protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                 IISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
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peptides of blood coagulation factor X. The role of the
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Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath
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actyla; Ruminantia; Pecora;
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       Proc. Natl. Acad.
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EGF-like module of blood coagulation:
spectroocopy and simulated folding.",
Biochemistry 31:5974-5983(1992).
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PTM: The vitamin K-dependent,
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PubMed=8794734;
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Sugo T., Bjoerk I., Holmgren A., Stenflo J.; "Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid-containing region."; Selander M., Persson E., Stenflo J., Drakenberg T.;
"IH NMR assignment and secondary structure of the Ca2(+)-free form
the amino-terminal epidermal growth factor like domain in coagulations versions." "Localization of the structural difference coagulation factors X1 and X2 to tyrosine 1 "How an epidermal growth factor (EGF)-like domain binds calcium. resolution NMR structure of the calcium form of the NH2-terminal combined NMR-small angle X-ray scattering study."; Biochemistry 35:11547-11559(1996). Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg The relative orientation of Gla and EGF domains actor X is altered by Ca2+ binding to the first converts prothrombin to thrombin in the presence of factor calcium and phospholipid during blood clotting CATALYTIC ACTIVITY: Preferential Cleavage: Arg-|-Thr and Arg-|-Ile bonds in prothrombin to form thrombin. SUBUNIT: The two chains are formed from a single-chain play the excision of two Arg residues and are held togethes another site, beyond the GLA domain. SIMILARITY: Belongs to peptidase fam INTRINSIC PATHWAY), OR BY FACTOR VIIA (I MISCELLANEOUS: Calcium also binds, with PTM: N- and O-glycosylated.
PTM: THE ACTIVATION PEPTIDE IS CLEAVED FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that SWISS-PROT entry is copyright. It is produced through a collaboration Belongs to peptidase family S1. Contains 2 EGF-like domains. to tyrosine 18 enzymatic carboxylation modified protein to bind apo form Stenflo J., Persson factor O BY FACTOR IXA (II)
(IN THE EXTRINSIC between bovine blood 18 in the activation 'n × stronger of the N-terminal X as determined by and the Teleman Drakenberg in coagulat EGF domain. coagulation -cnain precursor together by 1 o affinity bind 0; factor Va. EMBL outstation free form of coagulation Ü 얁 calcium PATHWAY) then H some ç MMR ç

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SMART; SM00179; EGF CA; 1.

SMART; SM001069; GLA; 1.

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PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS000022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS001147; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN LD; 1.
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InterPro; IPR009003 Cys_Ser_trypsin.
InterPro; IPR0090742 EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001438; EGF IIA.
InterPro; IPR001438; EGF IIA.
InterPro; IPR001438; EGF IIA.
InterPro; IPR002383; GLA_blood.
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Pfam; PF000594; gla; 1.
Pfam; PF000595; CYYPSin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLCOD.
PRINTS; PR00001; GLABLCOD.
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InterPro; IPR001254; P
InterPro; IPR001314; P
InterPro; IPR000294; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -|- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
-|- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.
-|- SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: N- and O-glycosylated (By similarity).
-!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).
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                                  FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
ACTIVATION PEDFILD.
ACTIVATED PACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTBNTIAL).
EGF-LIKE 2.
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MEDLINE=94318474; PubMed=8043441;
Murakawa M., Okamura T., Kamura T., Kuroiw
"A comparative study of partial primary st
region of mammalian protein C.";
Er. J. Haematol. 86:90-600(1994).
-!- FUNCTION: Protein C is a vitamin K-den
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                  SEQUENCE FROM N.A.
MEDLINE=97256311; PubMed=9101642;
Pendurthi U.R., Anderson K.D., Ja
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                             Coagulation
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                                                                               NCBI_TaxID=9986;
                                                                                                                               Oryctolagus cuniculus
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   "Characterization
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factor X precursor (EC 3.4.21.6)
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    of a full-length cDNA for rabbit factor
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us (Rabbit). Chordata; Craniata; Vertebrata; Eut Lagomorpha; Leporidae; Oryctolagus

Euteleostomi;

3.4.21.6) (Stuart

factor)

James H.L.;

PRT;

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Pfam; Frove....
PRINTS; PRO0722; CHYMOTKIFUL....
SMART; SM0020; Tryp_SPC; 1.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00136; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as use by non-profit institutions as long as i modified and this statement is not removed. Us
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulates blood coagulation by inactivating factors Va in the presence of calcium ions and phospholipids.
CATALYTIC ACTIVITY: Degradation of blood coagulation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Plasma; synthesized SIMILARITY: Belongs to peptidase family
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                            RQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGV 392
                                                                                                                                                                       EKWELDLDIEEVFIHENYTKSTTDNDIALLRLAQPATLSOTIVPICLPDSGLAERELTQA
                                                                                                                                                                                             EKWELDI.DIKEVFVHPNYSKSTTDNDIALI.HLAQPATI.SQTIVPICLPDSGLAERELNQA 291
RODACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGV
                                                                                     GOETLVTGWGYHSSREKEAKRNRTFILNFIKIPVVPRNECSEVMSNMVSENMLCAGILGD
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RESULT 6
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Vitamin.K-dependent protein C precursor (EC 3
(Autoprothrombin IIA) (Anticoagulant protein C
                                                                                                                                                                                                                                                                                                                                                                                            region
Br. J.
-!- FUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto "Isolation and characterization of a mouse protein J. Biochem. 11:491-495(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 274-434 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94318474; PubMed=8043441;
                                   This
                                                                                                                                                                                                                                 SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfice bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of andorhalical transcripts.
                                                                                                              strongly promoted by thrombomodulin.

TISSUE SPECIFICITY: Plasma; synthesized in the liver.

PIM: The vitamin K-dependent, enzymatic carboxylation of sresidues allows the modified protein to bind calcium.

MISCELLANEOUS: Calcium also binds, with stronger affinity another site, beyond the GLA domain. This GLA-independent site is necessary for the recognition of the thrombin-
                                                                                                                                                                                                                                                                                                                                     FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                 SIMILARITY: Belongs to peptidase family SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299
                                                                                                     thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                            of mammalian protein C.";
Haematol. 86:590-600(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSGGPMVVFFRGTWFLVGLVSWGEGCGHLNNYGVYTKVGSYLKWIHSYIGERDVSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSGGDWVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79:310-316(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1618739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwase R., Hashimoto-Gotoh T.;
of a mouse protein C cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sor (EC 3.4.21.69)
protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461
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binding
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the

European Bioinformatics

Institute.

There are no

restrictions

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PROSITE; PS00010; A
PROSITE; PS00022;
PROSITE; PS01186; E
PROSITE; PS50026; E
PROSITE; PS01187; E
PROSITE; PS00011;
PROSITE; PS00011; I
PROSITE; PS000134; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10445; BAA01235.1; -.
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MOD RES
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                        Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyglutamic acid; Calcium-binding; Vita
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002383; GLA blood.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001214; Peptidase S1A.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR009003; Cys_Set_trypsin.
InterPro; IPR0018a1; EGF_C.
InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS; S01.218; -. MGI:97771; Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P04070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF034569; AAC33795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM0 017
                                                                                                                                                                                                                                                                                                                                                          PS50240; TRYPSIN DOM;
PS00134; TRYPSIN HIS;
PS00135; TRYPSIN SER;
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10; ASX_HYDROXYL;
22; EGF_1; 1.
86; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF_CA; 1.
GLA; 1.
                                                                                                                                                                                                                                                                                                                                Repeat;
                                                                                                                                                                                                                                                                                                                                                                                        EGF CA; 1.
GLU_CARBOXYLATION;
                                                                                                                                                                                                                              33
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131
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461
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GLA_blood.
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                                                                                                                                                                                                                                                                                                                              id; Calcium-binding; Vitamin K; Hydroxylation;
Endothelial cell; Hydrolase; Signal.
                                                                                                                                                                                                                                                         PROTEIN C LIGHT CHAIN ()
PROTEIN C HEAVY CHAIN ()
ACTIVATION PEPTIDE (BY
CLEAVAGE (BY THROMBIN)
EGF-LIKE 1.
                   HYDROXYLATION (BY SIMILARITY)
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                       GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
                                                                              GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
                                                                                                                  GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
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                                                                                                          GAMMA-CARBOXYGLUTAMIC
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PEAM; PF00009; EGF; 2.

PEAM; PF00009; EGF; 2.

PEAM; PF00594; Gla; 1.

PEAM; PF00594; Gla; 1.

PEAM; PF00099; ETPSSIN; 1.

PEAM; PF000089; ETPSSIN; 1.

PRINTS; PR00001; GLABLOOD,

SMART; SM00109; EGF CA; 1.

SMART; SM00020; TTYP SPC; 1.

YOSITE; PS00010; ASK HYDROXYL; 1.

OSITE; PS00010; ASK HYDROXYL; 1.

OSITE; PS00010; EGF 3; 1.

STITE; PS01187; EGF TA; 1.

TTTE; PS01187; EGF TA; 1.

TTTE; PS01187; EGF TA; 1.

TTTE; PS01134; TRYPSIN HIS; 1.

TE; PS00134; TRYPSIN HIS; 1.

TE; PS00134; TRYPSIN SER; 1.

TOAGULATION; Glycoprotein; """
                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl S.
InterPro; IPR009003; Cys_Ser_trypsIn.
InterPro; IPR001881; EgF_Ca.
InterPro; IPR001881; EgF_Like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000184; VitK_dep_GLA.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way entities requires a license agreement '/o-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1131:329-332(1992).
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okafuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X64336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S18994; S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Autoprothrombin IIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium. MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Synthesized as a single chain precursor, which is cleave into a light chain and a heavy chain held together by a disulfice bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the presence of calcium ions and phospholipids.
CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reaction, which occurs at the surface of endothelial strongly promoted by thrombomodulin.
TISSUE SPECIFICITY: Plasma, synthesized in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and VIIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P04070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S01.218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is necessary for the recognition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Maekawa K., Nawa K., Marumoto Y.;
cloning and mRNA expression of rat protein C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA45617.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1PCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                   Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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EGF-like domain; Repea
SIGNAL 1 32
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                                                                                                                                                                                             Local
282
                 239
                                    222
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                                                                                                                                               42
                                                                                                                                                                                             Similarity
          | DIKEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVT
DIKEVLVHPNYTRSNSDNDIALLRLSQPATLSKTIVPICLPNSGLAQ-ELSQAGQETVVT
                                                                        APGYELADDHMHCRPTVNFPCGKLWKRTDKKRKNFKRDIDPEDEELELGPRIVNGTLTKQ
                                                                                   APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKR--DTEDQEDQVDPRLIDGKMTRR
                                                                                                            SPCCGHGTCIDGLGGFSCSCDKGWEGRFCQQEMGFQDCRVKNGGCYHYCLEETRGRRCRC
                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                 GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDL
                                                                                                                                                ANSFLEEVRAGSLERECMBEICDFEEAQEIFQNVEDTLAFWIKYFDGDOCSTPPLDHQCD
                                                                                                                                                                                                                        461 AA;
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42
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                                                                                                                                                                                                                        51912 MW;
                                                                                                                                                                                             71.2%;
69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid;
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                                                                                                                                                                                                                                                                                      CHARGE RELAY SYS
BY SIMILARITY.
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BY SIMILAR
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EGF-LIKE 2.
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PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY)
                                                                                                                                                                                   pred. No. 4.9e-
6; Mismatches
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GAMMA-CARBOXYGLUTAMIC
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PROSITE; PS0001; ASX HYDROXYL; 1.

PROSITE; PS00002; EGF 1; 1.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS00011; GLU CARBOXYLATION; 1.

PROSITE; PS000134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; FALSE NEG.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009903; Cys_Ser_trypSin.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001881; EGF Like.
InterPro; IPR002393; GIA_blood.
InterPro; IPR002383; GIA_blood.
InterPro; IPR001234; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR0001314; VitK_dep_GIA.
InterPro; IPR000294; VitK_dep_GIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strongly promoted by thrombomodulin.
-:- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
MOO RES
MOO RES
MOO RES
MOO RES
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MOO RES
                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SM00181; EGF; 2.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                    Gamma-carboxyglutamic
                                                                                                                                                                                                               Blood
                                                                                DOMAIN
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MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding another site, beyond the GLA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site is necessary for the recognition of the thrombin-
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                                                                                                                                                                                          .coagulation; Glycoprotein; Serine protease;
.coarboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
ike domain; Repeat; Endothelial cell; Hydrolase; Signal.
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  SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID.
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PROTEIN C HEAVY CHAIN.
ACTIVATION PEPTIDE.
EGF-LIKE 1.
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(Rel. 26, Last sequence update)
(Rel. 42, Last annotation update)
                                                                 STANDARD;
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71.3%;
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protein C precursor (EC 3.4.21.69)
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TGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACE
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10-OCT-2003 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3
(Autoprothrombin IIA) (Anticoagulant protein (page)
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MEDLINE-85014825; PubMed=6091100;

MEDLINE-85014825; PubMed=6091100;

Long G.L., Balagaje R.M., McGillivray R.T.A.;

Coning and sequencing of liver cDNA coding for bovine Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656 (1984).
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Bovidae; Bovinae; Bo
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                                                                                             MEDLINE=8321514; PubMed=6406503;
Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
"Structural changes required for activation of protein by Ca2+ binding to a high affinity site that does not c carboxyglutanic acid.";
J. Biol. Chem. 258:5554-5560(1983).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=83007326; PubMed=6896877; Stenflo J., Fernlund P.; Fernlund P.; Fernlund P.; Thinno acid sequence of the heavy chain of J. Biol. Chem. 257:12180-12190(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-83007325; PubMed-6896876; Fernlund P., Stenflo J.; Fernlund R., Stenflo J.; Tanion acid sequence of the light ch J. Biol. Chem. 257:12170-12179(1982)
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"Beta-hydroxyaspartic acid in vitamin K-dependent
Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
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FUNCTION: Protein C is a vitamin K-dependent serine pregulates blood coagulation by inactivating factors in the presence of calcium ions and phospholipids. CATALYTIC ACTIVITY: Degradation of blood coagulation and VIIIa.
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lt L.E., Esmon C.T.;
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                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
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Q9GLD2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vicamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood
      SEQUENCE FROM N.A.
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80.3%;
                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 5.36
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protein modeling of membrane binding
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MEDLINE=21121490; PubMed=11229814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Su or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF191307; AAG28380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. Mol. Life Sci. 58:148-159(2001).

FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Synthesized as a single chain precursor, which is cleaven to a light chain and a heavy chain held together by a disulfict bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues allows the modified protein to bind calcium.
MISCELLANEOUS: Calcium also binds, with stronger affinity to
another site, beyond the GLA domain. This GLA-independent bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strongly promoted by thrombomodulin.
TISSUE SPECIFICITY: Plasma; synthesized in the liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P04070;
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ding sites and
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SMART; SM00181; EGF; 2.

RMART; SM00181; EGF; 2.

SMART; SM00069; GLA; 1.

SMART; SM00069; TYPF\_SPC; 1.

SMART; SM00020; TYPF\_SPC; 1.

PROSITE; PS001016; ASX HYDROXYL; 1.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS001147; EGF CA; 1.

PROSITE; PS001147; EGF CA; 1.

PROSITE; PS001147; TRYPSIN DOM; 1.

PROSITE; PS001147; TRYPSIN DOM; 1.

PROSITE; PS001147; TRYPSIN SER; 1.

PROSITE; PS001147; TRYPSIN SER; 1. MEROPS, SO1.218; -.

InterPro; IPR00015; Asx hydroxyl\_S.

InterPro; IPR009003; Cys\_Ser\_trypsin.

InterPro; IPR009003; Cys\_Ser\_trypsin.

InterPro; IPR001881; EGP\_Ca.

InterPro; IPR001881; EGP\_Like.

InterPro; IPR001833; GLA\_blood.

InterPro; IPR001831; IESF.

InterPro; IPR001214; Peptidase\_S1.

InterPro; IPR001314; Peptidase\_S1A.

InterPro; IPR0001994; VitK\_dep\_GLA. PROPEP CHAIN CHAIN Gamma-carboxyglutamic acid; Calcium-binding. Serie protease; Gamma-carboxyglutamic acid; Calcium-binding. Series craw. PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00001; GLABLOOD. Pfam; SIGNAL Pfam; PP00008; EGF; 2. PF00594; gla; 1. PF00089; trypsin; 18 41 459 196 id, Calcium-binding, Vitamin K, Hydroxylation, Endothelial cell, Hydrolase, Signal. BY SIMILARITY.
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VITAMIN K-DEPENDENT PROTEIN C.
PROTEIN C LIGHT CHAIN (BY

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4
(Autoprothrombin IIIA) (Anticoagulant protein C)
factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIC I
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Submitted
-!- FUNCTI
residues allows the modified protein to bind calcium.

In MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

ENTITIARITY: Belongs to peptidase family $1.
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus
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                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
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                                                                                                            SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
                                                                                                                                                                                                                 n.L., He X., Dahlback B.;
mitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                        strongly promoted by Liromounders.
TISSUE SPECIFICITY: Plasma; synthesized in the liver.
                                                                                                                                                                                                  and VIIIa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLEDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                                                                                                                                                                                                                                                                                                                                                          cuniculus (Rabbit).
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Pred. No. 8.5e-176;
Mismatches 0;
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use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for our entities requires a linear a removed.
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                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 2 EGF-like domains.
                           EMBL; U49933; AAA92956.1; -.
P04070;
1PCU.
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SMART; SMODISI; EGF; 2.

SMART; SMODISI; EGF; 2.

SMART; SMODOSO; TLYP_SPC; 1.

SMART; SMODOZO; TLYP_SPC; 1.

PROSITE; PSODIOIO; ASX HYDROXYL; 1.

PROSITE; PSODIOIO; ASX HYDROXYL; 1.

PROSITE; PSODIOIO; EGF 7; 2.

PROSITE; PSODIOIO; EGF 7; 1.

PROSITE; PSODIOIO; EGF 7; 1.

PROSITE; PSODIOIO; EGF 7; 1.

PROSITE; PSODIOIO; EGF 7; 1.

PROSITE; PSODIOIO; TRYPSIN DOM; 1.

PROSITE; PSODIOIO; TRYPSIN HIS; 1.

PROSITE; PSODIOIO; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001881; I
InterPro; IPR006209; I
InterPro; IPR002383; InterPro; IPR006210; InterPro; IPR006210; InterPro; IPR001254; InterPro; IPR001254; I
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ACT_SITE
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PEPTIDE
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EGF-like domain; Repeat; Endothelial cell; Hv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood coagulation;
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PF00594; gla; 1.
PF00089; trypsin;
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Cys_Ser_trypsin.
EGF_Ca.
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GLA_blood.
IEGF.
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VitK_dep_GLA.
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Peptidase_S1A.
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BY SIMILAA...
BY SIMILARITY.
VITAMIN K-DEPENDENT PROTEIN C.
VITAMIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C LIGHT CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
TTAVAGE (BY THROMBIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                           id; Calcium-binding; Vitamin K; Hydroxylation;
Endothelial cell; Hydrolase; Signal.
                                                                                                                (BY SIMILARITY).

GAMMA-CARBOXYGLUTAMIC ACID

(BY SIMILARITY).

GAMMA-CARBOXYGLUTAMIC ACID

(BY SIMILARITY).
                                            GAMMA-CARBOXYGLUTAMIC A
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC A
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC A
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                    HYDROXYLATION
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                                (BY SIMILARITY)
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       SYSTEM
                   (BY SIMILARITY)
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MEDLINE-93190290; cu...
MEDLINE-93190290; cu...
Reitema P.H., Poort S.R., Berna...
Sala N., Cooper D.N.;
"protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C deficiency: a database of mutations. For the protein C defic
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"The 2.8 A crystal structure
EMBO J. 15:6822-6831(1996).
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"Characterization of a cD
proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation may influence the frequency
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"Beta protein C is not glycosylated at
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WEDLINE-07204221; PubMed=2437584;
Romeo G, Hassan H.J., Staempfili (
Leonardi A., Vicente V., Mannucci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92184750; PubMed=1544894;
Harris R.J., Ling V.T., Spellman
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"Hereditary thrombophilia: identifications in the protein C gene.";
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    VARIANT PROC DEPI
MEDLINE=91329836;
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                                                             "Protein C London 1: recurrent mutation at
the protein C gene causing thrombosis.";
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ked fucose is present in the first
of factor XII but not protein C.";
l. Chem. 267:5102-5107(1992).
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olie A., Talbot
      PubMed=1868249;
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                        CYS-272
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M., Bertina R.M., Pesci
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causing recurrent venous thrombosis.";
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deficiency caused by two mutant alleles,
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Gandrille S., Vidaud M., Aiach M., Alhenc-Gelas M., Fischer J
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CYS-328;
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        MEDLINE=93271396;
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CVS-328; ILE-385; THR-388 AND VAL-388
CVS-328; ILE-385; THR-388 AND VAL-388
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panel of 40 Dutch families with
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# OM protein - protein search, using sw model GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: June 2, 2004, 16:50:51; Search time 18 Seconds (without alignments) 1212.077 Million cell updates/sec

Title: US-09-997-623-4
Perfect score: 2324

Sequence: 1 ANSFLEELRHSSLERECIEE......LDWIHGHIRDKEAPQKSWAP 419

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

141681

141681 seqs, 52070155 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

3 3 3 2 2 5 6 6 6 7 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
1882.5 1756.5 1766.5 1654.5 1641.5 814.5 809.5 809.5 801.5 802.8 801.5 779.5 779.5 779.5 770.7 716.7 726.7 726.7 726.7 736.7 736.7 736.7 740.7 740.7 740.7 750.7 7	3 1 8
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490	455	625	275	699	638	638	271	275	396	400	655
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TMS2_MOUSE	TMS5_MOUSE	FA11_HUMAN	FA9_RABIT	CRAR_HUMAN	KAL HUMAN	KAL MOUSE	FA9_PIG	TRYT_PIG	PRTZ_BOVIN	PRTZ_HUMAN	HGFA_HUMAN
_	Q9er04 mus musculu	P03951 homo sapien	P16292 oryctoLagus	P48740 h complemen	P03952 homo sapien	P26262 mus musculu	P16293 sus scrota	Q9n2d1 sus scrofa	P00744 bos taurus	P22891 homo sapien	Q04756 homo sapien

## ALIGNMENTS

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SEQUENCE FROM N.A.  TISSUE-COlon;  MEDLINE-22388357; PubMed=12477932;  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  Bosak S.A., McEwan P.J., McEvernan K.J., Malek J.A., Gunaratne P.H.,  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,	MEDLINE-85269639; PubMed=2991859; BECURNARY R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R., Long G.L.; "The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs."; Nucleic Acids Res. 13:5233-5247(1985).  [3] SEQUENCE FROM N.A. MEDLINE-86120978; PubMed=3511471; Flutzky J., Hoskins J.A., Long G.L., Crabtree G.R.; Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).  [4] SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung MW., Lee K.L., Poel C.L., Yi Q., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  [5]	HUMAN STANDARD, PRT; 461 AA.  PO4070; Q15189; Q15190; Q16001; 01-MOV-1986 (Rel. 03, Created) 01-MOV-1986 (Rel. 03, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Vitamin-K-dependent protein C precursor (EC 3.4.21.69) (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).  PROC.  Budaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  MCBI_TaxID=9606; [1]

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A,Note: structure and location of a carbohydrate covalently bound to Ser C;Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, viramin K C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with struction:
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R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A;Reference number: A44556; MUID:89213999; PMID:3149637
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F;78,15,17,20,21,25,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #sta F;78,23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide F;53/Binding site: carbohydrate (Ser) (covalent) #status experimental F;64/Modified site: erythro-beta-hydroxyyaspartic acid (Asp) #status experimental F;158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental F;158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental F;222,270,366/Active site: His, Asp, Ser #status predicted
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                               2004, 16:57:37
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F;191-192/Cleavage site: Arg-Ala (Goagulation factor XIa) #status experimental F;203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental F;205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental F;226-227/Cleavage site: Arg-Val (Coagulation factor XIa) #status experimental
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A;Residues: 168-362, 'Q', 364-387, 'I', 389-451 <RES>
A;Residues: 168-362, 'Q', 364-387, 'I', 389-451 <RES>
A;Cross-references: GB:M26236; NID:g193319; PINN:AAA37630.1; PID:g193320
C;Comment: This protein plays a critical role in blood coagulation.
C;Comment: This protein factor; EGF homology; Gla domain homology; trypsin homology
C;Superfamily: coagulation factor; EGF homology; Gla domain homology; trypsin homology
C;Superfamily: coagulation acid; blood coagulation; calcium binding; carboxyglutam
C;Keywords: beta-hydroxysaspartic acid; blood coagulation; calcium binding; carboxyglutam
E;1-16/Domain: signal sequence (fragmen) #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: liver
R;Sarkar, G.; Koeberl, D.D.; Sommer, S.S.
Genomics 6, 133-143, 1990
A;Title: Direct sequencing of the activation
A;Reference number: I46580; MUID:90152675; PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 86, 275-278, 1990
A;Title: Deduced amino acid sequence of mouse blood-coagulation A;Reference number: JQ0419; MUID:90215309; PMID:2323576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision
C;Accession: JQ0419; I49667
R;Wu, S.M.; Stafford, D.W.; Ware, J.
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A; Residues: 1-459 < WUS>
                                         F;17-34/Domain: propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #status propeptide #stat
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNDFTRVVGGEDAKPGOFPWOVV-LNGKVDAFCGGSIVNEKWIVTÄÄHCVETGVKITVVA 279
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35.4%;
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F;225-452/Domain: trypsin homology <TRY>
F;41,42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) #st
F;52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-266,380-394,405-433/Dist
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                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 03-Aug-1984 #text_change 16-Jul-1999
C;Accession: A14757; B20274; I45891; A00923
C;Accession: A14757; B20274; I45891; A00923
R;Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie,
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                                                                                                                                             A;Molecule type: protein
A;Residues: 1-63,'T',65-416 <KAT'>
A;Residues: 1-63,'T',65-416 <KAT'>
B;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
B;Title: The occurrence of beta-hydroxyaspartic acid in
A;Reference number: A20274; MUID:83308813; PMID:6688525
A;Accession: B20274
                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A, Title: Comparison of amino acid sequence of bovine coagulation
A, Reference number: A14757, MUID:80056619; PMID:291916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation factor IXa (EC 3.4.21.22) N;Alternate names: Christmas factor
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A;Residues: 59-63,'X',65-69 <MCM>,R;Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G. Nature 299, 178-180, 1982
A;Title: Molecular cloning of the gene for human anti-b A;Reference number: I45891; MUID:82272386; PMID:6287289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                     A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LEBLRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEBFVRGNLERECIEERCSFEEAREVFENTEKTTEFWKQYVDGDQCESNP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPHNECSEVMSNIMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVTPIC----VANREYTNIFLKEGSG---YVSGWGKVENKGRHAS-----ILQYLRVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIVPICLPDSGLAERELNQ-----AGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPGDKIEVVAGEYNIDKKEDTEQRRNVIRTIPHHQYNATINKYSHDIALLELDKELILNS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNNVTESSESLNDFTRVVGGENAKPGOIPWOVI-LNGEIEAFCGGAIINEKWIVTAAHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQLAEDQKSCEPTVPFPCGRASISYSSKKITRAETVFSNMDYENSTEAVFIQDDITDGAI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKLGDDLLQCHPAVKFPCGRP------WKRMEKKRSH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDRATCLRS TTFTTYNNMFCAGYREGGKDS CEGDSGGPHVTEVEGTSFLTGI ISWGEECA
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Pred. No. 1.1e-45;
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  human anti-haemophilic PMID: 6287289
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A;Accession: 145891 A;Status: translated from A;Molecule type: mRNA

52-139

<CHO:

GB/EMBL/DDBC

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A;Residues: 1-193,'T',195-461 <JAY>
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611
A;Jaggdeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A;Title: Isolation and characterization of human factor IX cDNA: identification A;Reference number: A37546; MUID:84300528; PMID:8089357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: liver
R;Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A;Title: Development of an immunoaffinity process for factor IX purification.
A;Reference number: A60486; MUID:90194857; PMID:2316207
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                                                                                                                                                                                                                                                                                                                                                   A; Note: NMR detection of calcium binding by domain expressed in recombinant system R, de la Salle, C.; Charmantier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum, Thromb. Haemost. 70, 370-371, 1993
A;Title: A deletion located in the 3' non translated part of the factor IX gene responsi A; Reference number: 159612; MUID:94054330; PMID:8236150
A; Accession: 159612
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A; Residues: 1-12,'S',1
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A;Title: Isolation and characterization of a cDNA coding for human factor IX.
A;Reference number: A30623; MUID:83065193; PMID:6959130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 38-193,'T',195-326 <JAG>
A;Cross-references: GB:M35672
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A;Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
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A;Title: Genomic amplification with transcript sequencing. A;Reference number: 159529; MUID:88127096; PMID:3340835 A;Accession: 159529
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R;McMullen, B.A.;
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                                                                                                                            R;Stoflet, E.S.; Koeberl, I
Science 239, 491-494, 1988
                                                                                                                                                         A;Cross-references: GB:S66752; NID:9439773; PIDN:AAB28588.1; R;Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.
                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 444-461 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 9, 475-480, 1990
A,TItle: The first EGF-like domain from human factor IX contains a high-affinity calcium A;Reference number: S12377; MUID:90151623; EMID:2406129
A;Accession: S12377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: processed forms expressed in recombinant system
R;Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA; protein A; Residues: 1-68 < JAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 9, 3295-3301, 1990
A;Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: processed forms expressed in recombinant system R;Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien, EMBO J. 9, 3295-3301, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 29-63 <BAL>
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Eur. J. Biochem. 172, 565-572, 1988
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A; Residues: 105-109, 'X', 111-115 < MCM>
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A; Residues: 290-359 < RE2 >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 264, 21537-21265, 1989
A;Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan A;Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan A;Title: Blood clotting factor IX B(M) Nagoya
A;Reference number: A30622; MUID:90078229; PMID:2592373
A;Contents: annotation; sequence of mutant B(M) Nagoya
A;Note: carboxylation, glycosylation, and cleavage sites
A;Note: carboxylation, Glycosylation, and cleavage sites
A;Note: carboxylation, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
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J. Biol. Chem. 260, 2583, 1985
A;Reference number: A37544
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A; Residues: 'D', 2
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                                                                                                                                                                                                                                                                                                                                  F:29-46/Domain: propeptide #status experimental <PPT>
F;31-91/Domain: Gla domain homology <GLA>
F;47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F;97-128/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:119900; OMIM:306900
A;Map position: Xq27.1-Xq27.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-28/Domain: signal sequence #status predicted <SIG>
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A;Reference number: A18483; MUID:78194509; PMID:659613
A;Contents: annotation; activation; active site; carbohydrate binding R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984 A;Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623 R;Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; NB:g16emistry 33, 5567-5171, 1994 A;Residues: 'D',204,'X',206-211;212,'D',214,'X',216-221,'D' <AGA-A;Note: the residues designated 'X' were determined to be threonin R;Di\_Scipio, R.G.; Kurachi, K.; Davie, E.W. Biochemistry 33, 5167-5171, 1994
A;Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically line
A;Reference number: A54255; MUID:94227047; PMID:8172892 J. Clin. Invest. 61, 1528-1538, 1978
A; Title: Activation of human factor IX (Christmas factor). A;Status: translated from GB/EMBL/DDBJ pio, R.G.; Kurachi, K.; Davie, E.W. Invest. 61, 1528-1538, 1978 threonine bound to carbohydrate Y.; Nishimura, H.; Iwa Stafford,

R;Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5638-5704, 1984
A;Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding A;Reference number: A37543; MUID.84185715; PMID:6425296

Esmon, C.T.; Johnson, A.E.

A;Contents: annotation; calcium binding, correction

R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.

Cell 45, 343-348, 1986

Cell 45, 343-348, 1986

A;Title: Defective propeptide processing of blood clotting factor IX caused by mutation (A;Reference number: A37545; MUID:86189947; PMID:3009023

A;Reference number: A37545; MUID:86189947; PMID:3009023

A;Contents: annotation; signal second cleavage site

R;Suehiro, K; Kawabatta, S.I.; Miyatta, T.; Takeya, H.; Takamatsu, J.; Ogatta, K.; Kamiya, J. Biol. Chem. 264, 21257-21265, 1989

A;Note: recombinant form expressed in yeast C;Comment: Factor IX is activated by factor XIa, which excises the activation peptide proc;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K;C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strop

A; Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam A;Description: catalyzes the proteolytic activation of coagulation factor X in the prese pathway

F;134-170/Domain: EGF homology <EG2>
F;192-226/Domain: EGF homology <EG2>
F;192-226/Domain: activation peptide #status experimental <AHC>
F;227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;227-454/Domain: trypein homology <TRY>
F;227-454/Domain: trypein homology <TRYS
F;53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-435/D
F;949/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

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R;Axelrod, J.H.; Read, M.S.; Brinkhous, K.M.; Verma, I.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
A;Tille: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic A;Reference number: 146201; MUID:90311364; PMID:2367529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation factor IXa (EC 3.4.21.22) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Baccies: Canis lupus familiaris (dog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1991
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F;218-445/Domain: trypsin homology <TRY>
F;218-445/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,56,972,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;46,47,54,56,59,60,65,66,56,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di
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A; Residues: 1-452 < AXE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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.gritle: Molecular cloning of a cDNA encoding canine factor IX.
.greference number: A30351; MUID:89323338; PMID:2752110
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;90-121/Domain: EGF homology <EG1>
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 QVRHVAQLIMPDKYVPGKTDHDIALLRLLQPAALTNNVVPLCLPERNFSESTLATI-RFS 318
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                                                                                            PGYKLGDDLLQCHPAVKFPCGR---PWKRMEKKRSHLKRDTEDQEDQVD--
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                                                                                                                                                                   NDGVCKDDINSYECWCRAGFEGKNCELDVT---CNIKNGRCKOFC--KLGPDNKVVCSCT 151
                                TGYQLAEDQRSCEPAVPFPCGRVSVPHISMTRTRAETLFSNMDYENSTEVEKILDNVTQP 211
                                                                                                                                                                                                                                GHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRR----CSCA 121
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Pred. No. 2.1e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text_change 15-Sep-2000 C;Accession: A00922, A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A2 R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K. Biochemistry 24, 3736-3750, 1985 Biochemistry 24, 3736-3750, 1985 A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
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A;Residues: 1-193,'T',195.461 <MCG>
A;Cross-references: GB.M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
A;Cross-references: GB.M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
A;Note: the authors translated the codon ACA for residue 29 as Tyr
R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstoshé
Nucleic Acids Res. 11, 2325-2335, 1983
Mucleic Acids Res. 11, 2325-2335, 1983
A;Title: Isolation of a buman anti-haemophilic factor IX cDNA clone using a unique 52-baé
A;Reference number: A21337; MUID:83220788; PMID:6687940
                                                                                                                                                                                                                                                                                                   R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulating, Reference number: A22673; MUID:85190593; PMID:3857619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am. J. Hum. Genet. 45, 448-457, 1989
A;Title: Functionally important regions of the factor IX gene have a low rate of polymory
A;Reference number: A32989; MUID:89371752; PMID:2773937
A;Accession: A32989
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Blood 72, 1074-1076, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뭉
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A; Residues: 8-24 < REI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A37570; MUID: 84236100; PMID: 6329734
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                                                                                                                                                                                                                                                                              A; Accession: A22673
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-461 <ANS>
                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 LNDFTRVVGGKDAKPGQFPWQ-VLLNGKVDAFCGGSIINEKWVVTAAHCIEPDVKITIVA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 ---- PRLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 VSRYVNWI 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-92 <KOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -IADREYSNIFLKFGSG---YVSGWGRVFNKGRSAS-----ILQYLKVPLVDRATCLRST 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAERELNQ-----AGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEHNTEKREHTEOKRNVIRTILHHSYNATINKYNHDIALLELDEPLTLNSYVTPIC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.M.; Sommer,
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F;153-407/Product: coagulation factor VIIa heavy chain #status experimental <PAR2>
F;53-187/product: coagulation factor VIIa heavy chain #status experimental <PAR2>
F;67,714,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status F;17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/
F;52/Binding site: carbohydrate (Ser) (covalent) #status experimental #status experimental F;163/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental F;145,203/Binding site: carbohydrate (Asm) (covalent) #status experimental F;152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental F;193,242,344/Active site: His, Asp, Ser #status predicted F;193,242,344/Active site: His, Asp, Ser #status predicted
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R;McMullen, B.A.; Pujikawa, K.; Kisiel, W.
R;McMullen, B.A.; Pujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood A;Reference number: A20274; MUID:83308813; PMID:6688526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T. J. Biochem. 104, 867-868, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-407 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Bovine factor VII. Its purification and complete amino acid sequence. A;Reference number: A31979; MUID:89008362; PMID:3049594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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                                                                                                                                                                                                                                                                                       A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; ESF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-152/Product: coagulation factor VIIa light chain #status experimental <MAl>
F;1-44/Domain: Gla domain homology (fragment) <GLA>
F;50-81/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A31979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A31979; C20274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation factor VIIa (EC 3.4.21.21) - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Description: catalyzes the proteolytic activation of coagulation factor {\bf X} in the gulation factor {\bf I}{\bf X} in the presence of calcium and tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A;Reference number: A44556; MUID:89213999; PMID:3149637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 58-62, 'X', 64-68 < MCM>
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                                                                                                                                                                                                                                                            F;91-127/Domain: EGF homology <EG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: structure and location of covalently bound carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: C20274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, Chem. 263, 14868-14877, 1988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 GSKÓSCKGÓSGGPHATHYRGTWYĹTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
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                        179
                                                                                                                                                                                                                                                                                                                                                                                                                           168;
                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [46932
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F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S56300; NID:g266294; PID:g266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;24-83/Domain: Gla domain homology <GLA>
F;89-120/Domain: EGF homology <EG1>
F;130-166/Domain: EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coagulation factor VII - rabbit
C;Species: Cryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep_1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII A;Reference number: I46932; MUID:93190306; PMID:8383365 A;Accession: I46932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Brothers, A.B.; Clarke, Thromb. Res. 69, 231-238,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-443 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192-425/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
                                                                                                                                                                                                         94 -- CQNGGSCEDQIQSYICFCLADFEGRNCEKNKNDQLICMYENGGCEQYCSDHVGSQRSC 151
                                                                                                                                                                                                                                                                      61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVS-FLNCSLDNGGCTHYCLEEVGWRR-C 118
                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSPIEBLRHSSLERECIBBICDFEEAKEIFONVDDTLAFWSKHVDGDOCLVLPLEHPCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIH---GH 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVSGWGQLLERGVTARK-----LMVVLVPRLLTQDCLQQSRQRPGGPVVTDNMFCAGYSD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSN-----MVSENMLCAGILG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QERRVAQIIVPKQYVPGQTDHDVALLQLAQPVALGDHVAPLCLPDPDFADQTLAFV-RFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WCHEGYALQADGVSCAPTVEYPCGK-IPVLEKRNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPCQNGGSCEDQLRSYICFCPDGFEGRNCETDKQSQLICANDNGGCEQYCGADPGAGRPC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQRE-VSFLNCSLDNGGCTHYCLEEVG-WRRC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANGFLEELLPGSLERECREELCSFEEAHEIFRNEERTROFWVSYNDGDOC------AS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDLDIKEVFVHENYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQET 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GECPWQ-AMLKLNGALLCGGTLVGPAWVVSAAHCFERLRSRGNLTAVLGEHDLSRVEGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWE 235
                                                                    RCHEGYTLLENGVSCTPTVDYPCGKV-PALEKRGA-----SNPQGRIVGGKVCPK 200
                                                                                                                                 SCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRR 178
                                                                                                                                                                                                                                                                                                                                              ANSFLEELRPGSLERECKEELCSFEEAREVFQSTERTKQFWITYNDGDQCASNP-----
GDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDE---SKKLLVRLGEYDLRRWEKWE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
31-238, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.1%; Score 769.5; DB 2; 39.7%; Pred. No. 6.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 779.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.2e-49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SKPQGRIVGGHVCPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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A;Pathway: blood coagulation

G;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-40/Domain: propeptide #status predicted <PRO>

F;25-84/Domain: Gla domain homology <GLA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;129-167/Domain: EGF homology <EG2>
F;186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F;186-240/Domain: activation peptide #status predicted <APT>
F;241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;25-84/Domain: Ĝla domain homology <GLA>
F;41-185/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG2>
F;129-167/Domain: EGF homology <EG2>
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A;Molecule type: protein
A;Residues: 41-55 <GO2>
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C;Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C;Accession: A29322; A23819; A31186; B31186; S61524
C;Accession: A29322; A23819; A31186; B31186; S61524
R;O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뮍
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S20381
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                                                                                                                                                                                                          coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
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;441-468/Domain: trypsin homology <TRY>
;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)
;57-62,90-101,95-110,112,1129-140,136-152,154-167,175-348,247-252,267-283,396-410,
;57-62,90-101,95-110,112,129-140,136-152,154-167,175-348,247-252,267-283,396-410,
;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
;282,328,425/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                              380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 CSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRD-----TEDQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163;
                                                                                                                                                                                                                                                                                                                                                                 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 VLEVPYVDRSTCKQSTNFAITENMFCAGYETEQKDACQGDSGGPHVTRYKDTYFVTGIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 IHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHLAQPATLSQTIVPICLPDSGLAEREL-NQAGQETLVTGWGYHSSREKEAKRNRTFVLN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKLKEPIQFSEYVVPACLPQADFANEVLMNQ--KSGMVSGFGREFEAGRLSKR-----LK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNEDFILTAAHCINQSKEIKVVVGBVDREKEEHSETTHTAEKIFVHSKYIAETYDNDIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEVFTTTTESPTPPPRNGSSITDPNVDTRIVGGDECRPGECPWQAVLINEKGEEFCGGTI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSCTSGYELAEDGKQCVSKVKYPCGKVLMKRIKRSVILPTNSNTNATSDQDVPSTNGSIL 211
                                                                                                                                                                                                                                                                                                                                                                 WGEGCARKGKYGVYTKLSRFLRWVRTVMRQK 475
                                                                                                                                                                                                                                                                                                                                                                                                                       WGEGCGLLHNYGVYTKVSRYLDWIHGHIRDK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --CHYGGQCKDGLGSYTCSCLDGYQGKNCEFVIP-KYCKINNGDCEQFCSIKKSVQKDVV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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C;Genetics:
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A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations A;Reference number: A40529; MUID:91250411; PMID:1904059 A;Contents: annotation; carbohydrate binding sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;213-446()Product: coagulation factor VITa heavy chain #status experimental <MA2>
F;213-447/Domain: trypsin homology <TRY>
F;66,67,74,76,79,80,85,88,98/80/Modified site: gamma-carboxyglutamic acid (Glu) #status & F;77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-389,4 F;112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental F;123/Modified site: carbohydrate (Asn) (covalent) #status experimental F;23/Modified site: carbohydrate (Asn) (covalent) #status experimental
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J. Biol. Chem. 266, 11051-11057,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     F;212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental F;253,302,404/Active site: His, Asp, Ser #status predicted F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted
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A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
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A;Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
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A; Title: Structurally and functionally distinct Ca(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;110-141/Domain: EGF homology <EG1>
F;151-187/Domain: EGF homology <EG2>
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SICCGHGTCIDGIGSFSCDCRSGWEGRFCQ-REVSFINCSIDNGGCTHYCLEEVGWRR-C 118
                                                                                            ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQC--
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Pred. No. 7.
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R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation fact
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A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A21284; MUID:84222026; PMID:6587384
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R;Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of an almost full-length cDNA coding for human blood coagulati
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A; Residues: 13-284, 'E'
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A;Title: Isolation and characterization of human blood-coagulation factor X cDNA
A;Reference number: A25853; MUID:86221713; PMID:3011603
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C;Superfāmily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; c;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam F;1-2J/Domain: signal sequence #status predicted <SIG> F;24-40/Domain: bropeptide #status predicted <PRO> F;25-84/Domain: Gla domain homology <GLA>
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A,Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A,Reference number: A49458; MUID:93360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of C;Comment is the activation peptide is cleaved by factor IXa (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic pathway) of the IXA (in the intrinsic
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A;Accession: I54051
A;Status: translation not shown; translated from GB/EMBL/DDBJ
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A;Note: identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, (
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Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A;Reference number: S39414; MUID:94062825; PMID:8243461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A22208
                                                                                                                                                                                                                                                                                                                                    A,Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330 R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, J. Mol. Biol. 232, 947-966, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-23 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 84, 517-519, 1989

A, Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
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A; Residues: 183-234 < INO>
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                                                                                                                                                                                                                                                                                            A; Pathway: blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: deficiency of this factor causes Stuart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 13q34-13q34
A; Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:119890; OMIM:227600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:F10
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;Residues: 19-284,'E',289-488 <KAU>
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;Cross-references: GB:K03194, NID:g182840; PIDN:AAA52490.1; PID:g182841
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                                                                                                                                                                                                                                                                                                                                                                                                                Function:
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                                  A;Reference number: S20380; MUID:92164779;
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F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;133-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;133-234/Domain: activation peptide #status experimental <APT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid
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F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/I
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                                                             384
                                                                                                                                                                                                                                                                                                                                                                 270 YILTAAHCLYQAKREKVRVGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDEDIAVLRLK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ARGYTLADNGKACIPTGPYPCGK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQED-----
                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                                                                 205 WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIÄLLHLA 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSP----- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- CQNQCKCKDGLGEYTCTCLEGFEGKNCELFTRKL-CSLDNGDCDQFCHEEQNSVVCSC 151
                                                                                                                                                                                    PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG
                                                                                                                                                                                                                                                                                                           QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTENPFDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEF 269
      CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 479
                                                         CGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP 419
                                                                                                                          PYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEG
                                                                                                                                                                                                                                             TPITFRMNVAPACLPERDWAESTL--MTOXTGIVSGFGRTHEKGROSTR-----LKMLEV 382
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Pred. No. 9.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RLIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPS 204
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precursor - chicken

C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1993 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999
C;Accession: S15838; S20380; S20381 coagulation factor Xa (EC 3.4.21.6) precursor - N,Alternate names: virus-activating proteinase A;Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; R;Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y. FEBS Lett. 296, 274-278, 1992 A; Molecule type: mRNA A; Residues: 1-475 <SUZ> A; Title: Primary structure of the virus activating protease from chick embryo. Its ident: A; Reference number: S15838; MUID:91257322; PMID:2044767 R;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; ABaka, J.; Gotoh, B.; Ogasawara, FEBS Lett. 283, 281-285, 1991 A;Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible. A;Reference number: S20380; MUID:92164779; PMID:1537403 A;Accession: S15838 A; Status: not compared with conceptual translation PID:g222870

T.; Nag

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J. Biol. Chem. 264, 16897-16904, 1989
A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal A;Reference number: A34412; MUID:89380326; PMID:2789221
A;Accession: A34412
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A; Referen
A; Content
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A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 259, 5705-5740, 4204
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutami
A;Reference number: A38024; MUID:84185716; PMID:6546930
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R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo,
J. Biol. Chem. 259, 5705-5710, 1984
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R;Fujikawa, K.; Titani, K.; Davie, E.W.
R;Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Rtle: Activation of bovine factor X (Stuart factor):
A;Reference number: A13504; MUID:76053121; PMID:1059122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 11, 4899-4903, 1972
A;Title: Bovine factor X-la (activated Stuart factor). Evidence of homology with mammal
A;Reference number: A12453; MUID:73053314; PMID:4264286
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J. Biol. Chem.
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R;Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation; calcium binding R; Morita, T.; Jackson, C.M.
F;234-461/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) †
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) †
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
                                                                                                                                                                                                           F;129-164/Domain: EGF homology <EG2>
F;183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-233/Domain: activation peptide #status experimental <APT>
                                                                                                                                                                                                                                                                                                                                          F;41-180/Product: coagulation factor X light chain #status experimental F;90-121/Domain: BGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                       F;16-40/Domain: propeptide #status predicted <PRO>F;25-84/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Pathway: blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 13q34
                                                                                                                                                                  F;234-492/Product: coagulation factor Xa heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-15/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: F10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood; Reference number: A20274; MUID:83308813; PMID:6688526 (Contents: annotation; revision to residue 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Titani, K.; Pujikawa, K.; Enfield, D.L.; Bricsson, L.H.; Walsh, K.A.; Neurathroc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975; Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain; Reference number: Al2030; MUID:76053069; FMID:1059093
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,Residues: 183-196;199-209;216-233 <INO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r. J. Biochem. 218, 153-163, 1993
Title: Identification of O-linked oligosaccharide chains in the activation peptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Comment: Calcium binds to the gamma-carboxyglutamic acid residues arise by a posttranslational,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalyzes the proteolytic activation of prothrombin to thrombin in the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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F;200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental F;208,485/Binding site: carbobydrate (Thr) (covalent) #status experimental F;218/Binding site: carbobydrate (Asp) (covalent) #status experimental F;233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #statu F;240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental F;275,321,418/Active site: His, Asp, Ser #status predicted
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                                                 A;Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W. J. Biol. Chem. 267, 7395-7401, 1992 A;Title: Liver-specific expression of the gene coding for huma;Reference number: A42485; MUID:92218390; PMID:1313796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 15-Nov-1984 #sequence revision 02-May-1994 #text_change 08-Dec-2000 C;Accession: A24478; JQ0917; A42485; A25853; A22208; A21284; A20362; S39415 R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, B.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coagulation factor Xa (EC 3.4.21.6) N;Alternate names: Stuart factor
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A;Reference number: A42485;
A;Accession: A42485
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831
R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Gene for human Factor X: a blood coagulation factor whose gene A;Reference number: A24478; MUID:87026600; PMID:3768336
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                                                                                                                                                                                                                                  Gene 99, 291-294, 1991
A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coago
A;Beference number: JQ0917; MUID:91216473; PMID:1902434
A;Accession: JQ0917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 25,
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                                                                                                                                                                                      A; Residues: 1-488 < MES>
                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYVDRSTCKLSSSFTITPNMFCAGYDTQPEDACQGDSGGPHVTRFKDTYFVTGIVSWGEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPIRFRRNVAPACLPEKDWAEATL--MTQKTGIVSGFG-----RTHEKGRLSSTLKMLEV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPATLSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKI 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESSLDLLGLNRTEPSAGEDGSQVVRIVGGRDCAEGECPWQALLVNEENEGFCGGTILNEF 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGLLHNYGVYTKVSRYLDWI-----
                                                                                                                                                                                                               mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor [validated] - human
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                                                                                    coagula
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coagulation factor Xa (EC 3.4.21.6) precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Species: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000 C;Accession: S49075, UC4670; PS0191; PS0190; I62745 R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R. Thromb. Res. 80, 63-73, 1995
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A;Cross-references: EMBL:X79807; NID:g506600; June 1994
A;Note: submitted to the EMBL Data Library, June 1994
A;Note: neither the complete nucleic acid sequence nor the complete translation are sl R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: JC4670; MUID:96194815; PMID:8647460
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                                                                                                                                      C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam F;1-23/Domain: signal sequence status predicted <SIG>F;24-40/Domain: signal sequence status predicted <FRO>F;25-B4/Domain: Gla domain homology <GLA>F;25-B4/Domain: GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pl
A;Reference number: PS0190; MUID:92041742; PMID:1718949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Experimental source: Cos-1 cell
R;Enjyoji, K.; Miyazaki, K.; Kato, H.
F;41-179/Product: coagulation factor X light chain #status predicted <LCH> F;90-121/Domain: EGF homology <EG1> F;129-164/Domain: EGF homology <EG2> F;133-482/Product: coagulation factor X heavy chain #status predicted <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 295-383,'G',385-455 <NUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of
A;Reference number: I46196; MUID:94222160; PMID:8168596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 183-186, 'X', 188-207 <ENUZ>
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A;Molecule type: protein
A;Residues: 41-58,'X',60-65 <ENJI>
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A; Residues: 1-482 <STA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Murakawa, M.; Okamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PS0190
                                                                                                                                                                                                                                                                                                                                            A; Pathway: blood coagulation
                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I62745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;187/Binding site: carbohydrate (Asn) (covalent) #status experimental F;208/Binding site: carbohydrate (Thr) (covalent) #status predicted F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted F;231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;232-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #statt
F;57-62,90.101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41:
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   GKYGIYTKVTAFLKWIDRSMKARVGP
                                                        HNYGVYTKVSRYLDWIHGHIRDKEAP 413
                                                                                                                                                                                HNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLL 387
                                                                                                                                                                                                                                                                                                     LSQTIVPICLPDSGLAERELNQAGQET-LVTGWGYHSSREKEAKRNRTFVLNFIKIPVVP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SELLNLNKTEPEANSDDVIRIVGGQECKRGECPWQALLFSDEETDGFCGGTILNEFYILT 271
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                                                                                                                    RNTCRLSTSFSITQNMFCAGYDAKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARK 444
                                                                                                                                                                                                                                         FRENVAPACLPQKDWAEATL--MTQKTGIVSGFGRTHEKGRQSK-----VLKMMEVPYVD
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37.0%;
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RESULT 6

EXBO

Coagulation factor Xa (EC 3.4.21.6) precursor - bovine

coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N;Alternate names: Stuart factor

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1994 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999

C;Date: 24-Apr-1994 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999

C;Accession: A22867; A14997; A12030; A34412; S39414; A00925

R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.

Nucleic Acids Res. 12, 4481-4492, 1984

A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing

A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing

A;Reference number: A22867; MUID:84247315; PMID:6330671

A;Recession: A22867

A;Residues: 1-487 <FUN>
A;Residues: 1-487 <FUN>
A;Residues: 1-487 <FUN>
A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193

A;Coss-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g192; PIDN:CAA25286.1; PID:g192; PIDN:CAA25286.1; PID:g192; PIDN:CAA25286.1;

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F;43-461/Product: Protein C #status predicted <PRC>
F;91-130/Domain: EGF homology <BG1>
F;319-174/Domain: EGF homology <EG2>
F;213-445/Domain: Extypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;112/Modified site: erythro-beta-hydroxyaspartto acid (Asp) #status predicted F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disnlfide bonds: #status F;215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted F;254,300,402/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y. Biochim. Biophys. Acta 1131, 329-332, 1992
A;Title: The cDNA cloning and mRNA expression of rat protein A;Reference number: $24312; MUID:92329550; PMID:1627850
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A;Description: The cDNA cloninig and mRNA expression of rat protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S18994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;33-42/Domain: Gla domain homology <GLA>F;33-42/Domain: propeptide_#status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-461 < OKA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F;1-32/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S24312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963; Superfamily: coagulation factor X; EGP homology; Gla domain homology; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
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121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKR--DTEDQEDQVDPRLIDGKMTRR 178
                                            102
                                                                                      61
                                                                                                                                42
                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIKEVIIHPNYTKSTSDNDIALLRLAKPATLSQTIVPICLPDSGLSERKLTQVGQETVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIKEVFVHPNYSKSTIDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVT 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSGGPMVTFFRGTWFLVGLVSWGEGCGRLYNYGVYTKVSRYLDWIYGHIKAQEAPLESQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GWGYRD-
                                                                          SICCGHGTCIDGIGSESCDCRSGWEGRECQREVSEINCSIDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                  ANSFLEEVRAGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKYFDGDQCSTPPLDHQCD 101
                                                                                                                                                           ANSFLEELRHSSLERECIEEICDFEEAXEIFQNVDDTLAFWSKHVDGDQCLVLFLEHFCA
                                            SPCCGHGTCIDGLGGFSCSCDKGWEGRFCQQEMGFQDCRVKNGGCYHYCLEETRGRRCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456
                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                             71.2%; Score 1654.5; DB 1; 69.4%; Pred. No. 1.1e-113;
                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                  Length 461;
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                                                                                                                                                                                                                                                                                              Matches 291;
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                   Local Similarity
                           162
                                                                                                                  102
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121

APGYELADDHMRCKSTVNFPCGKLGRWIEKKRKILKRDT-DLEDELEPDPRIVNGTLTKQ

220

161

APGYKLGDDLLQCHPAVKEPCGREWKRMEKKRSHLKRDTEDQEDQV--DERLIDGKMTRR 178 SPCCGHGTCIDGIGSFSCSCDKGWEGKFCQQELRFQDCRVNNGGCLHYCLEESNGRRCAC 61 42 1

SLCCGHGTCIDGIGSESCDCRSGWEGRECQREVSPLNCSLDNGGCTHYCLEEVGWRRCSC 120

ANSFLEEURHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60

Conservative

57;

70.68;

Score 1641.5; Pred. No. 1e-1 Mismatches

1e-112; 67; DB 1;

Indels Length

ω ••

Gaps

ANSFLEEMRPGSLERECMEETCDFEEAQETFQNVEDTLAFWIKYFDGDQCSAPPLDHQCD 101

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F;212-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu)
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disnifide bond
F;214,290,355/Binding site: carbohydrate (Asp) (covalent) #status predicted
F;253,299,402/Active site: His. Asp. Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;139-174/Domain: EGF homology <EG2>
F;139-461/Domain: heavy chain #status predicted <PCH>
F;199-211/Domain: activation peptide #status predicted <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;34-41/Domain: propeptide #status predicted <PRO>
F;42-196,199-461/Product: protein C #status predicted <PRC>
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: liver C_1; Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that required the serine protein C is the zymogen of the vitamin K-dependent serine proteinase that required the serine protein C is the zymogen of the vitamin K-dependent serine protein C is the zymogen of the vitamin K-dependent serine protein C is the zymogen of the vitamin K-dependent serine protein C is the zymogen of the vitamin C-dependent serine protein C is the zymogen of the vitamin C-dependent serine protein C-dependent serine C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent C-dependent 
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A; Title: Isolation and characterization of a mouse protein C cDNA.
A; Reference number: JX0210; MUID:92316897; PMID:1618739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein C (activated) (EC 3.4.21.69) precursor - mouse N_{\rm r}Alternate names: vitamin K-dependent serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;27-85/Domain: Gla domain homology <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSGGPMVASFHGTWEIVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKS
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F;140-175/Domain: EGF homology <EG2>
F;140-175/Domain: EGF homology <EG2>
F;200-461/Product: protein C heavy chain #status experimental <APT>
F;200-211/Domain: ctivation peptide #status experimental <APT>
F;210-445/Domain: trypsin homology <TRY>
F;212-445/Domain: trypsin homology <TRY>
F;48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental F;02-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D F;06-111/Disulfide bonds: #status predicted
F;100/Binding site: carbohydrate (Thr) (covalent) #status absent
F;111/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;111-212/Cleavage site: Arg-Leu (thrombin) #status experimental F;211-212/Cleavage site: Arg-Leu (thrombin) #status experimental F;253,299,402/Active site: His, Asp, Ser #status predicted
F;125,253,299,402/Active site: His, Asp, Ser #status predicted
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A;Map position: 2q13-2q21
A;Map position: 2q13-2q21
A;Matrons: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C;Superfamily: cagulation; calcium binding; C;Reywords: anticoagulant; beta-hydroxysspartic acid; blood coagulation; calcium binding; F;1-32/Domain: signal sequence #status predicted <8IG>
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N.Alternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A18386; A0928
R;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5633-5656, 1994
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Accession: A26250; MUID:85014826; pMID:6091100
A;Accession: A26250
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;33-42/Domain: propeptide #status predicted <PRO>
;43-197/Product: protein C light chain #status predicted <LCH>
;22-131/Domain: EGF homology <EG1>
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100.0%; Pred. No. 1.
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1.1e-162;
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R;Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A;Title: Amino acid sequence of the heavy chain of bovine protein A;Reference number: A18386; MUID:83007326; PMID:6896877
A;Accession: A18386
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A,Residues: 197-494, 'PV' <STE>
A,Residues: 197-494, 'PV' <STE>
A,Residues: 197-494, 'PV' <STE>
A,Residues: 197-494, 'PV' <STE>
A,Residues: 197-494, 'PV' <STE>
A,Residues: 197-494, 'PV' <STE>
A,Residues: 197-494, 'PV' <STE>
J. Biol. Chem. 258, 5548-5553, 1983
J. Biol. Chem. 258, 5548-5553, 1983
A,Gontents: amnotation; activation; calcium binding
A,Gontents: amnotation; activation; calcium binding
A,Gontents: amnotation, activation; calcium binding
A,Gontents: amnotation, W.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
J. Biol. Chem. 258, 5554-5560, 1983
J. Biol. Chem. 258, 5554-5560, 1983
J. Biol. Chem. 258, 5554-5560, 1983
A,Title: Structural changes required for activation of protein C are induced by Ca2+ binc A,Reference number: A37542; MUID:83213514; PMID:86406503
A,Reference number: A37542; MUID:83213514; PMID:86406503
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A;Title: Amino acid sequence of the light chain of bovine protein
A;Reference number: A18385; MUID:83007325; PMID:6896876
A;Accession: A18385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cognition of the thrombin-thrombomodulin complex.

C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology (SKeywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>F;24-83/Domain: Gla domain homology <GLA>F;30-39/Domain: propeptide #status predicted <PRO>F;30-39/Domain: propeptide #status predicted <PRO>F;40-194/Product: protein C light chain #status experimental <LCH>F;40-194/Product: protein C light chain #status protein C light chain #status protein C light chain #status experimental <LCH>F;40-194/Product: protein C light chain #status protein C light chain #status protein C light chain #status protein C light chain #status prot
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A; Residues: 40-194 <FER>
A; Note: 82-Lys was also found
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R;Fernlund, P.; Stenflo, J.
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F;137-172/Domain: EGF homology <EG2>
F;137-456/Product: protein C heavy chain #status experimental <HCH>
F;197-456/Product: protein C heavy chain #status experimental <APT>
F;197-410/Domain: activation peptide #status experimental <APT>
F;211-440/Domain: trypsin homology <TRY
F;211-49/Domain: trypsin homology <TRY
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #status F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #status F;119/Modified site: expthro-beta-hydroxysepartic acid (Asp) #status experimental F;119-128, 137-148, 144-157,159-172,180-318,237-253,368-382,393-421/Dissifide bonds: #status F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Dissifide bonds: #status F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Dissifide bonds: #status F;119-128,159-128,144-157,159-172,180-318,237-253,368-382,393-421/Dissifide bonds: #status F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted F;252,298,397/Active site: His, Asp, Ser #status predicted F;252,298,397/Active site: His, Asp, Ser #status predicted
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                                                                                 160 APGYRLEDDHQLCVSKYTFPCGRLGKRMEKKRKTLKRDTNQVDQKDQLDERIVDGQEAGW 219
                                                                                                                                                                                                                                                                                                         100 LPCCGRGKCIDGLGGFRCDCAEGWEGRFCLHEVRFSNCSAENGGCAHYCMEEEGRRHCSC 159
                                                                                                                                                                                                                                                                                                                                                                                                             61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
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                                                                                                                                                                                                APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTE--DQEDQVDPRLIDGKWTRR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Mismatches
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Maximum DB seq length: 200000000
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1641.5
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1: pir1:*
2: pir2:*
3: pir3:*
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NUMBER OF SEQ ID NOS: 12

SOFTMARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens

US-10-182-263-3
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                                                                                     361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                                                              301 GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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                                                               361 GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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Search completed: June Job time : 50 secs

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
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PRIOR APPLICATION NUMBER: 60/181948
PRIOR EILING DATE: 2002-02-11
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CURRENT APPLICATION NUMBER: US/10/182,263
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Pred. No. 9.3e-188;
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US-10-182-263-3

Sequence 3, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611

CURRENT APPLICATION NUMBER: US/10/182,263

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RESULT 14
US-10-168-407-6
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CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 419
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TITLE OF INVENTION: PROTEIN C DERIVATIVES
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                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQXSWAP
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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Pred. No. 1.4e-187;
3; Mismatches 3;
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US-10-670-628-2
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CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NDS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
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APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
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Publication No. US20030207435A1
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                                             Sequence 2, Application US/10670628 Publication No. US20040038288A1 GENERAL INFORMATION:
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APPLICANT: Huang, Lihua
APPLICANT: Riggin, Ralph
TITLE OF INVENTION: HUMAN
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Local Similarity 98.8%;
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CURRENT APPLICATION NUMBER: US/10/670,628
CURRENT FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 2
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                   GGPMVASPHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQK 415
                                                                    GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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RESULT 12
US-10-168-407-5
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Publication No. US20030207435A1
                                                                         Matches
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Best Local
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SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Jones, Bryan E
TITLE DF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: X-13610
                                                                                                                                                                   LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
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                     1 ANSFLEELRHSSLERECIEBICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 60
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ANSFLEELROGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKHVDGDQCLVLPLEHPCA
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; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-168-407-2
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Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerilitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE DEPENDENCE. V 1992
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Publication No. US20030022354A1
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION UNMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                 CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
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CURRENT PILING DATE: 2002-07-22
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                                                                                                                                                                            FILE REFERENCE: X-13610
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 4.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-3
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Publication No. US20030207435A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING PARE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                        Local Similarity
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Pred. No. 1.3e-188;
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Pred. No. 4.2e-190;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
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TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CHAIN
LOCATION: (43)...(461)
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TITLE OF INVENTION: Protein C or activated pr
FILE REFERENCE: 0219us410 - protein C
CURRENT APPLICATION NUMBER: US/09/997,623
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 09/978,917
PRIOR APPLICATION NUMBER: US 09/978,917
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver: 2.1
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SIGNAL
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Similarity 100.0%;
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No. US20030018175A1
                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVFHNECSEVMSNMVSENMLCAGILGDRQDACEGDS 360
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                           GGPMVASPHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWLHGHIRDKEAPQKSWAP 419
                                                                      GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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RESULT 7 US-10-182-263-2

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US-10-182-263-1
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Best Local S
Matches 419
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Publication No. US20030018175A1

GENERAL INFORMATION: Maxygen Holdings

APPLICANT: Maxygen Aps; Maxygen Holdings

TITLE OF INVENTION: Protein C or activated protein C-like molecules

FILE REFERENCE: 0219us410 - protein C

CURRENT APPLICATION UNMERS: US/09/997,623

CURRENT FILING DATE: 2001-11-29

CURRENT FILING DATE: 2001-11-29
Sequence 1, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce B
APPLICANT: Jones, Bryan E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
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PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
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TYPE: PRT
ORGANISM: Homo sapiens
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Similarity 100.0%;
19; Conservative 0
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Pred. No. 3.8e-190;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER: OF SEQ ID NOS: 12
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RESULT 4
US-10-168-407-1
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ORGANISM: Homo sapiens
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                                                                                                            GGPMVAS FHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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                                                                                GGPMVASFHGTWPLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
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Sequence 1, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 100.0%; Score 2324; DB 15; Length 419; Best Local Similarity 100.0%; Pred. No. 3.8e-190; Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB-pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB-pep:*

14: /cgn2 6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

15: /cgn2 6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

17: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

18: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-997-623-4
2324
1 ANSFLEELRHSSLERECIEE.....LDWIHGHIRDXEAPQKSWAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 2, 2004, 16:55:32; Search time 48 Seconds (without alignments) 2455.852 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1155919 seqs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	Query Match Length DB	ength	BB	ID	Description	
1	2324	100.0	419	10	US-09-978-917A-4	Sequence 4,	Appli
N	2324	100.0	419	12	US-09-997-623-4	Sequence 4,	Appli
ω	2324	100.0	419	14	US-10-182-263-1	Sequence 1,	Appli
4.	2324	100.0	419	15	US-10-168-407-1	Sequence 1,	Appli
ഗ	2324	100.0	461	10	US-09-978-917A-2	Sequence 2,	Appli
σ	2324	100.0	461	12	US-09-997-623-2	Seguence 2,	Appli
7	2324	100.0	461	14	US-10-182-263-2	Seguence 2,	Appli
œ	2324	100.0	461	15	US-10-168-407-2	Seguence 2,	Appli
9	2306	99.2	419	15	US-10-168-407-3	Seguence 3,	Appli
10	2302	99.1	419	15	US-10-168-407-4	Seguence 4,	Appli
11	2298	98.9	415	12	US-10-670-628-2	Seguence 2,	Appli
12	2298	98.9	419	15	US-10-168-407-5	Seguence 5,	Appli
13	2296	98.8	419	14	US-10-182-263-5	Sequence 5,	Appli
14	2294	98.7	419	15	US-10-168-407-6	Seguence 6,	Appli
15	2290	20	419	14	115-10-182-263-3	Seguence 3.	1

45	44	43	42	41	40	39	38	37	36	35	3. <u>4</u>	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
736	736	739	740	741.5	746	749.5	758.5	775.5	777	779	779.5	782	783	783	783	783	783	783	783	783	783	783	783	783	803	803	809	2286	2288
31.7	31.7	31.8			32.1	32.3	32.6	33.4	33.4	33.5	33.5	33.6	33.7	33.7	33.7	33.7		33.7		33.7				33.7		34.6		œ	98.5
461	456	456	461	437	488	437	453	455	467	405	454	467	467	466	466	444	444	444	444	444	444	406	406	406	488	488	488	419	419
9	16	16	16	12	12	12	12	12	12	15	12	12	12	15	14	16	16	16	12	12	12	16	15	10	14	14	12	14	14
US-09-884-901-3	US-10-038-854-95	US-10-038-854-96	-10-038-854-	US-10-712-332-3	US-10-712-332-1	-332-	US-10-406-031-14	-031-	-10-406-	US-10-360-101-225	-10-406-031-1	0-406-031	US-10-406-031-8	US-10-375-741-14	US-10-017-122-2	US-10-263-205B-3	-10-411	US-10-410-962-8	US-10-411-026-8	US-10-382-248-34	US-10-411-037-8	US-10-263-205B-2	US-10-383-898-1	US-09-782-587B-3	US-10-407-123-27	US-10-348-504-44	US-10-406-031-27	US-10-182-263-4	US-10-182-263-6
Sequence 3, Appli	Sequence 95, Appl	96,	Sequence 94, Appl	GENERAL INFORMA	GENERAL INFORMA	LIN	14,	17,	2, Appl	22	11	ហ	æ -	14	'n	w -	9	8	æ	34	8	2	۲	ū	Sequence 27, Appl	Sequence 44, Appl	e 27	Sequence 4, Appli	Sequence 6, Appli

### ALIGNMENTS

Ma Ma	DЬ	γQ	
Best Local Similarity 100.0%; Pred. No. 3.8e-190; Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	61 SLCOGHGTCIDGIGSFSCDCRSGWEGRFCOREVSFINCSIDNGGCTHYCLEEVGWRRCSC 120 121 APGYKLGDDLLOCHPAVKFPCGRFWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 180	SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC APGYKLGDDLLQCHPAVKFPCGRPWKRWEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD	SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC APGYKLGDDLLQCHPAVKFPCGRFWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
	1 ANSPLEEIRHSSIERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDOCLVLPLEEHCA 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQRSFLNCSLDNGGCTHYCLEEVGWRRCSC 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 121 APGYKLGDDLLQCHPAVKFPCGRPWKMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD	1 ANSPLEELRHSSIERECTEEICDFEEAKEIFQNVDDPTAFWSKHVDGDOCLVLPLEHPCA 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 121 APGYKLGDDLLQCHPAVKFPCGRPWKRWEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD 121 APGYKLGDDLLQCHPAVKFPCGRPWKRWEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD	1 ANSPELEILHILLICHPERAKEIFONVODPILAFWSKHVOGDOCLVLPLEHPCA 1 ANSPELEILHILLICHPERAKEIFONVODPILAFWSKHVOGDOCLVLPLEHPCA 61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
QY 1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60	61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC	61 SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC	61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLFLEHPCA 	61 SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 121 APGYKLGDDLLCQCHPAVKFPCGRPWKXMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD	61 SLCCGHGTCLDGIGSESCDCRSGWEGRFCCREVSFINCSLDNGGCTHYCLBEVGWRRCSC 121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD	61 SLCCGHGTCIDGIGSESCDCRSGWEGRFCQREVSFINCSLDNGGCTHYCLEEVGWRRCSC 121 APGYKLGDDLQCHPAVKFPCGRPWKRNEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA	121 APGYKLGDDLLQCHPAVKFPCGRPWXXMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD	121 APGYKLGDDLLQCHPAVKFPCGRPWKRNEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD	121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA		121 APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKWTRRGD	121 ABGYKLGDDLLQCHPAVKFPCGRPWKWBKKRSHLKKDTEDQEDQVDPRLIDGKMTRRGD 181 SPWQVVLLDSKKKLACGAVLTHPSWVLTAAHCWDESKKLAVRLGBYDLRRWEKWLDLDLDI

Murray MJ,

Berkner KL,

Foster DC;

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Query Match
Best Local Similarity 100.
Matches 419; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein C (AAW02600) is a zymogen of a serine protease that plays an important role in the regulation of blood coagulation and the generation of fibrinolytic activity in vivo. It is synthesised in the liver and processed to a 2-chain molecule, which is itself converted to activated protein C. Protein C and activated protein C are useful in the treatment of thrombotic disorders. They can be produced e.g. in mammalian host cells using a cDNA clone (AAT32795) derived from Hep G2 cells. Variant protein C, modified to improve cleavage between the heavy and light chains of the circulating intermediate, can also be produced. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-251006/25.
N-PSDB; AAT32795, AAT32796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 2A-C; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-thrombotic agent.
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Local Similarity 100.0%;
403
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                         GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                           GYHSSREKEAKRIRTEVLNEIKIPVVPHNECSEVMSNWVSENMLCAGILGDRQDACEGDS
                                                                                                                                       GYHSSREKEAKRURTFYLINFIKIPVYPHNECSEYMSINWSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                     KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 300
                                                                                                                                                                                                                                                                                                                                                              SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                 APGYKLGDDLLQCHPAVKFPCGRPWKKMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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  GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 461
                                                                                                                                                                                                                KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
                                                                                                                                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 3.3e-143;
; Mismatches 0;
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Search completed: June Job time : 63 secs

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AAW02600
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  Disulfide-bond
                          Disulfide-bond
                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW02600;
                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                            Activated protein C; serine protease; thrombosis; thrombolytic; fibrinolytic; antithrombotic; blood clotting; therapy.
                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
05-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agent or a fibrinolysis promoter
                                                                                                        Disulfide-bond
                                                                                                                                   Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                     Human protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW02600 standard; protein;
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                                                                                                                                                              Disulfide-bond
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Local Similarity 100.0%; I
hes 419; Conservative O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPNVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRODACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
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                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
 /note=
122
                                                    /note=
                                                                              /note= "forms
                                                                                                                                  /note= "forms disulphide bond with Cyslll"
                          120
                                                                                                          105
                                                                                                                                                                                                                    /label= Pre-pro-peptide
43. .461
                                      /note= "forms disulphide bond with Cys92"
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                     'note= "fors disulphide bond with Cys105"
                                                                                                                                                                                                   /label= Mat_protein
                                                                                                                                                                          'label= GLA_domain
              "forms
                                                               "forms disulphide bond with Cys120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2324; DB 2;
Pred. No. 3.3e-143;
); Mismatches 0;
           disulphide bond with Cys106'
                                                                                         disulphide bond with Cys101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 461;
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29-CCT-1986;

08-DEC-1987;

28-FEB-1989;

10-SEP-1990;

04-DEC-1992;
                                                                                                      27-JUN-1985;
                                                                                                                                 08-APR-1994;
                                                                                                                                                            14-MAY-1996.
                                                                                                                                                                                     US5516650-A
                                                                                                                                                                                                                              Disulfide-bond
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           ( OMYZ)
           ZYMOGENETICS INC
                                   85US-00749600.
86US-00924462.
87US-00130370.
89US-00317205.
90US-00582131.
92US-00987532.
                                                                                                                               94US-00225253.
                                                                                                                                                                                                                                                        /note=
398
                                                                                                                                                                                                                                                                                 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "residues 198-199 are replaced by Lys-Lys or Arg-
Arg in constructs of the invention"
198. .199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "residue 196 is replaced by Lys, Arg
constructs of the invention"
197. .198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  254
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/note= "cleavage site between connecting dipeptide and
activation peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "forms disulphide bond with 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "residue 200 is replaced by Ala, Ser, in constructs of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198. .199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "forms disulphide bond with Cys122'
138
                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                        note= "forms disulphide bond with Cys426"
                                                                                                                                                                                                                                                                                                                      'label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                       'label= N-glycosylation_site
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                                                                                                                                                                                                                                                                                             note= "forms disulphide bond with Cys387"
                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "forms disulphide bond with Cys238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "forms disulphide bond with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "cleavage site for activation peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= Activated_protein-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "cleavage site for connecting dipeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "forms disulphide bond with Cys319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "forms disulphide bond with Cys162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "forms disulphide bond with Cys140"
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                                                                                                                                                                                                                                                                                                                                                 label= N-glycosylation_site
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                                                                                                                                                                                                               "forms disulphide bond with Cys 398"
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                                                                                                                                                                                                                                                                                                                                                                              Cys183"
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                                                                                                                                                                                                                                            The sequence was deduced from a clone isolated from a cDNA library prepd. CC from mRNA from Hep G2 cells. It is a protein C precursor, including light CC and heavy chains, which is clasved to produce activated protein C (see CC feature table). The DNA encoding the sequence can be manipulated by contivated a comprising techniques to express a protein comprising (when activated) a heavy chain and a truncated light chain comprising residues CC 1-149, 1-150, 1-151 or 1-152 of the natural sequence. The protein pref. CC comprises the precursor of formula: Pre-pro-L-X-H Pre-pro = pre-pro peptide of protein C with all/part replaced by the corresponding peptide of either protein S, factors VI, IX or X, or prothrombin; L = AAs 1-149, CC 150, 151 or 152 of light chain; X = 3-10 Lys/arg residues; and H = heavy CC chain. Cells transformed with expression vectors contg. the modified DNA CC sequences produce the new proteins which can be used to regulate anticoagulant and fibrinolytic systems. See also W09112320 (AARI3074). CC (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                              Query Match
Best Local S
Matches 419
                                                                                                                                                                                                                                          Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant protein C with truncated light chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-222903/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foster DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO) ZYMOGENETICS INC. (TEIJ ) TEIJIN LTD.
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   163
                             121
                                                           103
                                                                                                                                                                                419;
                                                                                      61
                                                                                                                    43
                                                                                                                                                  μ
                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ12649
                         APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                          SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                              SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                                        ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                              ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holly RD,
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139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label=
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                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteolytic cleavage
                                                                                                                                                                             Score 2324; DB 2;
Pred. No. 3.3e-143;
; Mismatches 0;
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                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1991;
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A human protein C or an activated protein C has a H chain contg. one of the residues 239-246 (= residues 450-457 in the sequence below) in the H chain of natural activated protein C as the C-terminal, or has a L chain contg. one of the residues 141-155 (= residues 141-155 in the sequence below), pref. residues 149-155 (= residues 149-155 in the sequence below), the L chain of natural activated protein C as the C-terminal. The

human protein

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or the

activated protein

C can be used as an anticlotting

Human protein C and activated protein C with short H chains - useful anti-clotting agents and fibrinolysis promoters.

3 13

Disclosure; Fig 1; 8pp; Japanese.

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This sequence, or a fragment of it, is used in the construction of hybrid phospholipid-binding proteins (PBP) having the same biological activity as human protein C or human activated protein C. The hybrid sequence would comprise at least one lipocortin phospholipid binding domain (PBD), e.g. of PAP-1, joined to a gla-domainless protein C or activated protein C. See AAQ12680-81 for such examples. See also AAQ12678-81. (Updated on
  Sequence 461 AA;
                                                                                                                      Recombinant prodn. of hybrid phospholipid-binding proteins - comprising lipocortin phospholipid-binding domain and vitamin=K-dependent protein.
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30-SEP-1991
                      25-MAR-2003
                                                                                                  Disclosure; Fig 2; 57pp; English.
                                                                                                                                                               WPI; 1991-222905/30.
                                                                                                                                                                                    Foster DC;
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Query Match
Best Local Similarity
Matches 419; Conserv
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/label= gamma carboxyglutamic acid
                                                                     /label= gamma carboxyglutamic acid 67
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43. .197
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                                                   'label= gamma carboxyglutamic acid
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htive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 4 - 7; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA encoding zymogen form of human protein C - and its activated deriv., useful as e.g. antithrombotic agents more sensitive to thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the protein sequence of nascent human protein C encoded by the
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 461
                                                                                                   GYHSSREKEAKRNRTFVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                      Matches 419;
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Best Local Similarity
                                                                                                                                                                                                                                                                           The amino acid sequence codes for human protein C (HPC). The activated protein can comprise one of 3 different truncated light chains, Ala(1) to Lys(150), Lys(151) or Arg(152). The activated HPC with a truncated light chain is more stable during storage. It can be administered for prophylactic and/or therapeutic treatments of disease states or injuries to enhance the patient's own anti- coagulative or fibrinolytic capabilities. See also W09109951 (AARI3074). (Updated on 25-WAR-2003 to
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TEIJIN LTD.
                                   ANSFLEELRHSSLERECIEBICDFEBAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 60
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RESULT 9
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     Murray MJ,
                                                                                       27-JUN-1985;
15-AUG-1985;
                                                                                                                                                                                                             EP215548-A.
                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
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                                                                                                                                        26-JUN-1986;
                                                                                                                                                                          25-MAR-1987.
                                                                                                                                                                                                                                                            Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Protein
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10-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP70855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70855 standard; protein; 461 AA
                                    (ZYMO ) ZYMOGENETICS INC. (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343
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   Berkner KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                     85US-00749600.
85US-00766109.
                                                                                                                                        86EP-00304970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= prepro leader peptide 59. .64
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "apparent dipeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183. .319
/note= "links together the two processed chains"
197. .198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199. .200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                            /label= N-glycosylation site 373. .387
                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-coagulant; thrombosis; serine protease.
                                                                                                                                                                                                                                                                                                               label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "apparent processing site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= growth factor domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= gamma-carboxyglutamic acid
92. .175
                                                                                                                                                                                                                                                                                                                                                  'label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                   "in heavy chain; converts
     Foster
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     Davie
     EW;
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RESULT 10
AAP90401
ID AAP90
XX AAP90
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XX 25-MA
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DT 25-MA
C AAP90
XX Engag
XX Human
XX Human
XX Human
XX Homo
XX Engag
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Best Local 9
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                                                                                                                                                                                                                                        25-MAR-2003
01-NOV-1989
                                                                                                                                                   Human protein C; zymogen form; activated C protein; human liver mRNA; signal peptide; propeptide; antithrombotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1987-081505/12.
N-PSDB; AAN70102.
                22-DEC-1988;
                                                  05-JUL-1989
                                                                                   EP323149-A.
                                                                                                                    Homo sapiens
                                                                                                                                                                                                      Zymogen form of human protein C.
                                                                                                                                                                                                                                                                                             AAP90401;
                                                                                                                                                                                                                                                                                                                            AAP90401 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%;
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                                                                                                                                                                                                                                        (revised)
(first entry)
                88EP-00312201
                                                                                                                                                                                                                                                                                                                              461
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Recombinantly produced protein C can be used to treat thrombotic disorders such as venous thrombosis as it has anti-coagulant properties. The protein sequence is thought to yield two peptide chains; the first contains the Gla domain and growth factor domains and the second (the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein \mathbb C or activated protein \mathbb C - prepd. using expression vector capable of integration in mammalian host cell DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vation peptide contains the catalytic domain.
to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLEELRHSSLERECIEEICDEEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                        GYHSSREXEAKRNRTFVLNFIKIPVVPHNECSEVMSNWVSENMLCAGILGDRQDACEGDS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                       APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD 180
                                                                                                                                                                      KEVFVHPNYSKSTTDNDIALIHLAQPATLSQTTVPICLPDSGLAERELNQAGQETLVTGW
                                                                                                                                                                                                                                                                                               SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SICCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSBVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                           KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW 342
                                                                                                                                                                                                                                                      SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKNELDLDI
                                                                                                                                                                                                                                                                                                                                                                                     APGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2324; DB 1;
Pred. No. 3.3e-143;
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RESULT 7
APP81104
ID APP8
XX AAP8
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XX Homo
XX Homo
XX JP63
XX 21-4
XX 21-4
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N-PSDB; AAN81408.
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GGPMVAS.FHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                                                                                                              GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                       GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 3.3e-143;
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25-JUL-1991
                                                                                                                                                                                                                                                                                                                                             Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of polypeptide having human protein C activity - is by recombinant DNA procedures for prod. useful against vascular disorders.
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GYHSSREKEAKRIRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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                                                                                                                                                                                   SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRCSC
                                                                                                                                                                                                                                    ANSFLEBLRHSSLERECIBEICDFBEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA 102
                                            KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAEREINQAGQETLVTGW 300
                                                                             SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDI
                                                                                                  SPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVR1GEYDLRRWEKWELDLDI
                                                                                                                               APGYKLGDDLLQCHPAVKFPCGRPWKRMEXKRSHLKRDTEDQEDQVDPRLIDGKMTRRGD
                        KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                         100.0%; Score 2324; DB 1; 100.0%; Pred. No. 3.3e-143; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification describes a chimeric protein, based on protein C, which comprises a thrombin-cleavable artificial sequence. This artificial sequence is of a formula given in the specification, and comprises a peptide from fibrinopeptide A, and a thrombin-cleavage site, other than that of the alpha-chain of fibrinogen. The chimeric protein and serine protease derivatives obtained by cleaving the chimeric protein with thrombin, are useful as antithrombotic, antiinflammatory, antiapoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and profibrinolytic agents, for treatment or prevention of hypercoagulative diseases, e.g. venous and arterial thrombosis; myocardial infarction; pulmonary embolism; reocclusion after angioplasty and alterations in the genes for protein C and thrombomodulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the mature form of human protein C. protein is an essential factor in the regulation of coagglation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric protein, cleavable by thrombin, useful e.g. as antithrombotic agents, particularly modified protein C containing artificial activation sequence.
                                                          ADC40014 standard;
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                                                                                                                        GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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Matches 419;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a pharmaceutical composition containing protein C (aPC), a chelating agent and optionally a diluent. The composition of the invention is useful for treating thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical composition comprising activated protein C and a agent useful for treating thrombotic disorders such as stroke, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intravascular coagulation; thrombotic stroke; deep pulmonary embolism; peripheral arterial thrombosis;
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                                GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
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                                                                                             GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
                                                                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVNSNNVSENMLCAGILGDRQDACEGDS
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                                                                                                        KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2324; DB 7
100.0%; Pred. No. 3e-143;
tive 0; Mismatches 0
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Human Protein C zymogen protein
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Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; seps1s; sept1c shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin.

### Homo sapiens

WO200232461-A2.	Peptide	Protein	Peptide	Key Protein
	158169 /label= Activation_peptide	158419 /label= Heavy_chain	/Iabel≡ Light_chain 156157 /lahel≡ Lvs Ard dimemtide	Location/Qualifiers 1155

## 25-APR-2002

15-OCT-2001; 2001WO-DK000679.

18-OCT-2000; 2000DK-00001560. 18-OCT-2000; 2000US-0242268P. 21-JUN-2001; 2001DK-00000970. 21-JUN-2001; 2001US-0300154P.

(MAXY-) MAXYGEN APS.
MAXYGEN HOLDINGS LTD

Andersen KV, AH, Freskgaard PO;

## 2002-489875/52.

N-PSDB;

Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.

# Claim 2; Page 79-81; 92pp; English

cc attachment group for the non-polypeptide group (e.g. an N-glycosylation occ site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least CC 5% of its side group exposed to the surface, with the provise that the cc substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln.

Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VI) comprising (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-cc life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and cdiagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow crashitatory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 correased resistance reduced immunogenicity and/or increased beavailability. The conjugate offers a number of advantages over the currently available configurate offers a number of advantages over the currently available. The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an

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                      GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                                        GYHSSREKEAKRNRT FVLNFIKI PVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                         GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSBNMLCAGILGDRQDACEGDS
                                                                                                                                                     KEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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Pred. No. 3e-143
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ABR55547 standard; protein; 419

ABR55547;

11-AUG-2003 (first entry)

Amino acid sequence of mature human protein C (PC).

Protein C, coagulation, thrombin; fibrinopeptide A, serine protease; antithrombotic; antiinflammatory; antiapoptotic; profibrinolytic; hypercoagulative disease; thrombosis; myocardial infarction; pulmonary embolism; reocclusion; angioplasty; thrombomodulin.

Homo sapiens

25-APR-2003 Region Active-site Region FR2831170-A1 158. .169 170. .419 Location/Qualifiers /note= "light chain" .157

19-OCT-2001; 2001FR-00013492

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RESULT 3
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Matches 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001
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type activated human protein C. They also have longer half-lives in human
blood and hence require either less frequent administration and/or
smaller dosage than wild type human protein C for treating disorders
                                                                                                               11-FEB-2000; 2000US-0181948P.
14-MAR-2000; 2000US-0189199P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mature wild type protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE08625;
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                                                                                                                                                                                                                                                                    16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                     (ELIL ) LILLY & CO ELI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               prothrombotic disorder; gene therapy; thalassaemia
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Pred. No. 3e-143;
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Gerlitz BE,

Grinnell BW,

Jones

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RESULT 4 AAU99002

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23-AUG-2002 AAU99002; AAU99002

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemorlytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein c deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arterials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increase sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or in vascular grafts in combination with a thrombolytic agent. Nucleic molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human mature wild type protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
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                           GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP 419
                                                                                                     GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGIIGDRQDACEGDS 360
                                                                                                                                                                                            KEVFYHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGW
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GGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQKSWAP
                                                                                GYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDS
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Pred. No. 3e-143;
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Sequence 419 AA;
            coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                                   resistance to inactivation by serpins compared with wild-type human protein C but retain the biological activity of the wild-type protein.
                                                                                                                                                                                                                                        The present sequence is that of human protein C mature polypeptide. The invention relates to human protein C derivatives having at least 2 amino acid substitutions, and to recombinant DNA molecules encoding such derivatives. These derivatives have increased anticoagulant activity and
                                                                                                                                                                                                                                                                                                                    Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                  Claim 1; Page 49-50; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001; 2001WO-US000020.
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-2000; 2000US-0179801P.
14-MAR-2000; 2000US-0189197P.
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                                                                                                                                                                                                                                                                                                                                                                                                     Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-glycosylated"
331. .345
356. .384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "activation peptide; removal activates the 2-chair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-glycosylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "thrombin cleavage site"
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1 ANSFLEELRHSSLERECIEEICDFEEAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA

69

uremic syndrome, and also useful acute coronary syndromes such as

unstable angina

Query Match Best Local S Matches 419

Similarity

100.0%; Score 2324; DB 4 100.0%; Pred. No. 3e-143; tive 0; Mismatches 0

DB 4; 0;

Length Indels

419; 0; Gaps

419;

Conservative

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AAB36894
ID AAB
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 The present invention relates to a human protein C derivative. The protein is useful for treating vascular occlusive disorders, hypercoagulable states such as sepsis, disseminated intravascular coagulation, purpura fulminans, major trauma, major surgery, burns, adult respiratory distress syndrome, transplantation, deep vein thrombosis, heparin-induced thromboytopenia, sickle cell disease, thalassemia, viral hemorrhagic fever, thrombotic thromboytopenic purpura, and hemolytic uremic syndrome, and also useful for treating thrombotic disorders and uremic syndrome, and also useful for treating thrombotic disorders and
                                                                                                                                                                                                      Protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states
                                                                                                                                                          Claim 1; Page 42-44; 57pp; English.
                                                                                                                                                                                                                                                                N-PSDB; AAC83311.
                                                                                                                                                                                                                                                                                                                  Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000
                                                                                                                                                                                          predisposing thrombosis, comprises specific amino
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                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocardial infarction; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickie cell; thalassemia; thrombotic disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein C derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36894;
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Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1586107 seqs, 282547505 residues
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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### SUMMARIES

Result	Score	% Query Match	Length DB	₩.	ID	Description	ion
L .	2324	100.0	419	. 4	AAB 82 673	Aab82673	Wild-type
2	2324	100.0	419	4.	AAB36894	Aab36894	Human pro
ω	2324	100.0	419	4.	AAE08625	Aae08625	Human mat
4.	2324	100.0	419	G	AAU99002	Aau99002	
ъ	2324	100.0	419	6	ABR55547	Abr55547	
σ,	2324	100.0	419	7	ADC40014	Adc40014	
7	2324	100.0	460	_	AAP81104	Aap81104	Sequence
80	2324	100.0	461	Н	AAP60001	Aap60001	Sequence
9	2324	100.0	461	_	AAP70855	Aap70855	Human Pro
10	2324	100.0	461	Н	AAP90401	Aap90401	Zymoqen f
11	2324	100.0	461	N	AAR13622	Aar13622	Human pro
12	2324	100.0	461	N	AAR13081	Aar13081	Human pro
13	2324	100.0	<b>4</b> 61	N	AAR13074	Aar13074	Protein C
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16	2324	100.0	461	N	AAY49561	Aay49561	
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18	2324	100.0	461	4	AAB36895	Aab36895	
19	2324	100.0	461	4	AAE08626	Aae08626	Human wil
20	2324	100.0	461	u	AAU99001	Aau99001	Human Pro
21	2321	99.9	419	Ģ	AAU99035	Aau99035	
22	2321	99.9	419	u	AAU99031	Aau99031	
23	2321	99.9	461	_	AAP81205	Aap81205	
24	2321	99.9	461	_	AAP90070	Aap90070	
25	2320	99.8	419	л	A 21100 174	Aau99074	

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99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.8	99.8	99.8	
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AAU99019	AAU99013	AAW25086	AAU99043	AAU99075	AAU99036	AAU99069	AAU99047	AAR35760	AAR13584	AAR13585	AAR13582	AAR13997	AAU99032	AAU99096	AAU99073	AAB36896	AAR13539	AAU99015	AAU99033	
	Aau99013	Aaw25086	Aau99043	Aau99075	Aau99036	Aau99069	Aau99047	Aar35760	Aar13584	Aar13585	Aar13582	Aar13997	Aau99032	Aau99096	Aau99073	Aab3 6896	Aar13539	Aau99015	Aau99033	
Human	Human	Human	Human	Human	Human	Human	Human Pro	Protein C	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	
						Pro	Pro	C III.				pro	-	Pro	_	pro	_	1 Pro	Pro	

### ALIGNMENTS

	DOW LA  LA  LA  LA  LA  LA  LA  LA  LA		FT Key FT Domain FT Modifi FT Modifi FT Modifi FT Modifi		RESULT 1 AAB82673 ID AAB XX AC AAB XX DT 15
Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond	Modified-site Modified-site Modified-site	Modified-site Modified-site Modified-site Modified-site	Key Domain Modified-site Modified-site	Wild-type human Protein C; human Myocardial infa myocardial yrotein sepsis; protein antibacterial; anticoagulant; Homo sapiens.	T 1 673 AAB82673 standa AAB82673; 15-CCT-2001 (f
/note= "N-glycosylated" 50. 69 59. 64 80. 89 98. 1109 120. 133 141. 277 156157	<pre>/note= "gamma-carboxylated" 25 /note= "gamma-carboxylated" 26 /note= "gamma-carboxylated" 29</pre>	/note= "O-phosphorylated"  1	Location/Qualifiers 145 /note= "Gla domain" 6 /note= "gamma-carboxylated" /note= "gamma-carboxylated" 12		Standard; protein; 419 AA.;

### US 102764430IP1



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Indexing Officer: SUK - SOPHY UK

Team: OIPEBackFileIndexing

Dossier: 10276443

Legal Date: 07-16-2004

No.	Doccode	Number of pages
1	CTFR	7

Total number of pages: 7

Remarks:

Order of re-scan issued on .....